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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:20:09 ; Search time 92.6283 Seconds
(without alignments)
1101.172 Million cell updates/sec

Title: SEQ29_1-172_990-1178
Perfect score: 1850
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1833.8	99.1	373	3	AA53624	Aay53624 A bone ma
2	1833.8	99.1	373	3	AA56969	Aay56969 Human MAG
3	1833.8	99.1	373	3	AAB24242	Aab24242 Human Nog
4	1833.8	99.1	373	4	AAB82350	Aab82350 Human NOG
5	1833.8	99.1	373	5	AAM47954	Aam47954 Human RTN
6	1833.8	99.1	373	5	ABP68601	Abp68601 Human pan
7	1833.8	99.1	373	5	ABB81079	Abb81079 Human neu
8	1825.8	98.7	373	5	ABG30937	Abg30937 Human Nog
9	1756.9	95.0	1192	3	AA56967	Aay56967 Human MAG

10	1756.9	95.0	1192	4	AAB82349	Aab82349	Human	NOG
11	1756.9	95.0	1192	4	AAU04591	Aau04591	Human	Nog
12	1756.9	95.0	1192	5	ABG30938	Abg30938	Human	Nog
13	1756.9	95.0	1192	5	ABP68600	Abp68600	Human	pan
14	1756.9	95.0	1192	5	ABB81078	Abb81078	Human	neu
15	1756.9	95.0	1192	6	ABR59667	Abr59667	Human	Nog
16	1749.3	94.6	1178	3	AAY71311	Aay71311	Human	neu
17	1556.2	84.1	379	7	ADB85283	Adb85283	Rat	fooce
18	1551.6	83.9	361	3	AAY71385	Aay71385	Alternati	
19	1549.3	83.7	359	3	AAY71558	Aay71558	Rat	Nogo
20	1546.3	83.6	360	3	AAY71383	Aay71383	Rat	neuri
21	1546.3	83.6	360	5	ABB81076	Abb81076	Rat	neuro
22	1480.5	80.0	360	4	AAE03987	Aae03987	Human	gen
23	1478.8	79.9	1163	3	AAY71310	Aay71310	Rat	neuri
24	1478.8	79.9	1163	3	AAY71384	Aay71384	Alternati	
25	1478.8	79.9	1163	5	ABB81074	Abb81074	Rat	neuro
26	1476.8	79.8	1162	3	AAY71557	Aay71557	Rat	Nogo
27	1475.2	79.7	1246	4	AAU33228	Aau33228	Novel	hum
28	1324.8	71.6	291	4	AAM93484	Aam93484	Human	pol
29	1028	55.6	893	3	AAY95012	Aay95012	Human	sec
30	1028	55.6	983	6	ABU11573	Abu11573	Human	MDD
31	993.5	53.7	642	2	AAW58383	Aaw58383	Human	sec
32	993.5	53.7	642	4	AAB90682	Aab90682	Human	BG1
33	967.3	52.3	403	3	AAY71563	Aay71563	Rat	Nogo
34	938.2	50.7	200	4	AAB64514	Aab64514	Human	sec
35	932.9	50.4	284	3	AAY95030	Aay95030	Human	clo
36	927	50.1	199	2	AAW53947	Aaw53947	Human	NSP
37	927	50.1	199	2	AAW78313	Aaw78313	Fragment	
38	927	50.1	199	3	AAB12805	Aab12805	Human	NSP
39	927	50.1	199	4	AAB82348	Aab82348	Human	NOG
40	927	50.1	199	5	ABB81080	Abb81080	Human	neu
41	918	49.6	199	2	AAY35903	Aay35903	Extended	
42	906	49.0	199	3	AAY71559	Aay71559	Rat	Nogo
43	904	48.9	199	5	ABB81077	Abb81077	Rat	neuro
44	904	48.9	522	3	AAY71312	Aay71312	Rat	neuri
45	886	47.9	199	5	ABG30939	Abg30939	Human	Nog

ALIGNMENTS

RESULT 1

AAAY53624

ID AAAY53624 standard; protein; 373 AA.

XX

AC AAAY53624;

XX

DT 22-FEB-2000 (first entry)

XX

DE A bone marrow secreted protein designated BMS112.

XX

KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;

KW cell proliferation; cell differentiation; hematopoiesis; anaemia;

KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;

KW erythroid progenitor cell; colony stimulating factor; granulocyte;

KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;

KW platelet disorder; thrombocytopenia; hematopoeitic stem cell;

KW stem cell disorder; aplastic anaemia; bone differentiation;
KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
KW bone fracture; cartilage damage; artificial joint.

XX

OS Homo sapiens.

XX

PN WO9933979-A2.

XX

PD 08-JUL-1999.

XX

PF 18-DEC-1998; 98WO-US027008.

XX

PR 30-DEC-1997; 97US-0068958P.

PR 24-SEP-1998; 98US-0101603P.

PR 30-SEP-1998; 98US-0102540P.

XX

PA (CHIR) CHIRON CORP.

XX

PI Lin H, Cao L;

XX

DR WPI; 2000-038344/03.

DR N-PSDB; AAZ36230.

XX

PT New isolated human polynucleotide and secreted proteins can induce
PT production of other cytokines in certain cell populations.

XX

PS Claim 2; Page 74; 120pp; English.

XX

CC AAY53622-43 represent bone marrow secreted proteins of human bone marrow
CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or
CC cell differentiation activity (either inducing or inhibiting). They can
CC be used to support colony forming cells or factor-dependent cell lines,
CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell
CC deficiencies. In addition, they may be used to support the growth and
CC proliferation of erythroid progenitor cells, and to treat various
CC anaemias. They can have colony stimulating factor (CSF) activity and can
CC be used to support the growth and proliferation of myeloid cells such as
CC granulocytes, monocytes or macrophages, to prevent or treat myelo-
CC suppression, to support the growth and proliferation of megakaryocytes
CC and platelets, thereby allowing prevention or treatment of platelet
CC disorders such as thrombocytopenia, to support the growth and
CC proliferation of hematopoietic stem cells, either in place of or in
CC conjunction with platelet transfusions, to treat stem cell disorders,
CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
CC repopulate the stem cell compartment after irradiation or chemotherapy.
CC They can be used for growth or differentiation of bone, cartilage,
CC tendon, ligament, or nerve tissue, as well as for wound healing and
CC tissue repair and replacement, and in the treatment of burns, incisions
CC and ulcers, to induce cartilage and/or bone growth in circumstances where
CC bone is not normally formed and thus have an application in healing bone
CC fractures and cartilage damage or defects, prophylactic use in fracture
CC reduction and also in the improved fixation of artificial joints

XX

SQ Sequence 373 AA;

Query Match

99.1%; Score 1833.8; DB 3; Length 373;

Best Local Similarity 96.5%; Pred. No. 1.5e-64;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60
      |||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120
      |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTS----- 173
      |||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
      |||
Db    181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240

Qy    229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 288
      |||
Db    241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 300

Qy    289 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
      |||
Db    301 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360

Qy    349 IQAKIPGLKRKAE 361
      |||
Db    361 IQAKIPGLKRKAE 373

```

RESULT 2

AAAY56969

ID AAY56969 standard; protein; 373 AA.

XX

AC AAY56969;

XX

DT 25-APR-2000 (first entry)

XX

DE Human MAGI polypeptide variant.

XX

KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW psychiatric disorder; developmental disorder; inflammatory disorder;
KW stroke; cytostatic; cerebroprotective; neuroprotective; variant.

XX

OS Homo sapiens.

XX

PN WO200005364-A1.

XX

PD 03-FEB-2000.

XX

PF 21-JUL-1999; 99WO-GB002360.

XX

PR 22-JUL-1998; 98GB-00016024.

PR 19-JUL-1999; 99GB-00016898.

Db 361 IOAKIPGLKRKAE 373

RESULT 3

AAB24242

ID AAB24242 standard; protein; 373 AA.

XX

AC AAB24242;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human Nogo B protein sequence SEQ ID NO:2.

XX

KW Human; Nogo B; cell stress response; hyperphosphorylated; brain tumour;

KW stress-phosphorylated endoplasmic reticulum protein; cytostatic;

KW gene therapy; cell growth; cellular stress response; neuron growth;

KW regulator of oxidative stress; inhibitor of neurite outgrowth;

KW axon regeneration; diagnosis; cancer; identification.

XX

OS Homo sapiens.

XX

PN WO200060083-A1.

XX

PD 12-OCT-2000.

XX

PF 07-APR-2000; 2000WO-US009383.

XX

PR 08-APR-1999; 99US-0128372P.

PR 21-JUN-1999; 99US-0140331P.

XX

PA (CHIR) CHIRON CORP.

XX

PI Wei D, Halenbeck R, Williams LT;

XX

DR WPI; 2000-665007/64.

DR N-PSDB; AAC64406.

XX

PT Novel protein associated with cell stress response useful for modulating

PT stress levels, cell growth, diagnosis and treatment of cancer and

PT malignant growth and for identifying agonists and antagonists.

XX

PS Claim 11; Fig 1A; 68pp; English.

XX

CC The present sequence represents a human stress-phosphorylated endoplasmic

CC reticulum protein, designated Nogo B. Nogo B has cytostatic activity and

CC is a modulator of the storage and exchange of calcium, cell growth and

CC cellular stress response. It can: regulate oxidative stress; inhibit

CC neurite outgrowth, neuron growth and axon regeneration. Nogo B

CC polypeptides and polynucleotides are useful for modulating stress levels

CC and cellular stress-response, cell growth and viability, diagnosis and

CC treatment of cancer, malignant growth and other Nogo B related diseases.

CC Nogo B polypeptides are also useful to screen combinatorial libraries to

CC identify agonist or antagonist. Antibodies against Nogo B polypeptides

CC are useful for affinity chromatography and distinguishing Nogo B

CC polypeptides

XX

SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 3; Length 373;
 Best Local Similarity 96.5%; Pred. No. 1.5e-64;
 Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

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Qy      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      |||
Db      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
      |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTS----- 173
      |||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
      |||
Db    181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240

Qy    229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 288
      |||
Db    241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 300

Qy    289 KFAVLMWVFTTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
      |||
Db    301 KFAVLMWVFTTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360

Qy    349 IQAKIPGLKRKAE 361
      |||
Db    361 IQAKIPGLKRKAE 373
  
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RESULT 4

AAB82350

ID AAB82350 standard; protein; 373 AA.

XX

AC AAB82350;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human NOGO-B protein.

XX

KW NOGO-B; human; chromosome 2p21; neuropathy; spinal injury; brain injury;

KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;

KW neuromuscular disorder; psychiatric disorder; developmental disorder;

KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;

KW cerebroprotective; neuroleptic; diagnosis; therapy.

XX

OS Homo sapiens.

XX

PN WO200136631-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-GB004345.

XX

PR 15-NOV-1999; 99GB-00026995.
PR 24-JAN-2000; 2000GB-00001550.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.

XX
PI Michalovich D, Prinjha R;

XX
DR WPI; 2001-343822/36.

DR N-PSDB; AAF90325.

XX

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
PT gene and may be useful in the treatment of neural disorders including
PT Alzheimer's and Parkinson's diseases.

XX

PS Disclosure; Page 27-38; 25pp; English.

XX

CC The present sequence is that of human NOGO-B. NOGO-B is a previously
CC known splice variant of the human NOGO gene on chromosome 2p21. The
CC invention relates to a novel splice variant, NOGO-C (see AAB82348). It
CC provides NOGO-C polypeptides and polynucleotides, and methods for
CC producing such polypeptides by recombinant techniques. Also disclosed are
CC methods for utilising NOGO-C polypeptides and polynucleotides in the
CC treatment of diseases including neuropathies, spinal injury, brain
CC injury, stroke, neuronal degeneration, for example Alzheimer's disease
CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders
CC and developmental disorders. Also provided are methods for identifying
CC agonists and agonists for use in treating conditions associated with NOGO
CC -C imbalance, and diagnostic assays for detecting diseases associated
CC with inappropriate NOGO-C activity or levels

XX

SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 4; Length 373;
Best Local Similarity 96.5%; Pred. No. 1.5e-64;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

Qy 1 MEDLDQSPVLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
|
Db 1 MEDLDQSPVLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP 120
|
Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP 120

Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTS----- 173
|
Db 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG 180

Qy 174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
|
Db 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240

Qy 229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 288
|
Db 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 300

Qy 289 KFAVLMWVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348

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Db          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 KFAVLMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360

Qy          349 IQAKIPGLKRKAE 361
          ||||||||||||
Db          361 IQAKIPGLKRKAE 373

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RESULT 5

AAM47954

ID AAM47954 standard; protein; 373 AA.

XX

AC AAM47954;

XX

DT 04-MAR-2002 (first entry)

XX

DE Human RTN4B SEQ ID NO 4.

XX

KW Human; RTN4B.

XX

OS Homo sapiens.

XX

PN CN1311439-A.

XX

PD 05-SEP-2001.

XX

PF 02-MAR-2000; 2000CN-00111791.

XX

PR 02-MAR-2000; 2000CN-00111791.

XX

PA (UYFU-) UNIV FUDAN.

XX

PI Yu L, Fu Q, Zhao Y;

XX

DR WPI; 2002-049934/07.

DR

N-PSDB; ABA05903.

XX

PT Human RTN 4B protein and coding sequence, its preparation and use.

XX

PS Claim 5; Page 11 (Disclosure); 27pp; Chinese.

XX

CC The invention relates to human RTN4B protein and coding sequence, useful
 CC for providing a cDNA sequence of human RTN4B. The protein is an isomer of
 CC RTN4 with RTN family members. The present invention also refers to
 CC polypeptide encoded by a nucleotide sequence and manufacturing method and
 CC application of the polypeptide and polynucleotide

XX

SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 5; Length 373;

Best Local Similarity 96.5%; Pred. No. 1.5e-64;

Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

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Qy          1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
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Db          1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

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XX
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 XX
 DR WPI; 2002-627435/67.
 DR N-PSDB; ABV94681.
 XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic
 PT cancer.
 XX
 PS Claim 2; SEQ ID NO 72; 300pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 5; Length 373;
 Best Local Similarity 96.5%; Pred. No. 1.5e-64;
 Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60
 |||
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60

 Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
 |||
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

 Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTS----- 173
 |||
 Db 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

 Qy 174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
 |||
 Db 181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240

 Qy 229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 288
 |||
 Db 241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 300

 Qy 289 KFAVLMWVFTYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348

```

Db      301 KFAVLMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360
Qy      349 IQAKIPGLKRKAE 361
      |||||
Db      361 IQAKIPGLKRKAE 373

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RESULT 7

ABB81079

ID ABB81079 standard; protein; 373 AA.

XX

AC ABB81079;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo-B.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; human; receptor.

XX

OS Homo sapiens.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;

PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86601.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.

XX

PS Example; Page 56-57; 93pp; English.

XX

CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its

CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease is
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents the human
 CC neurotransmitter receptor protein Nogo-B, an example of NS-specific
 CC antigen
 XX
 SQ Sequence 373 AA;

Query Match 99.1%; Score 1833.8; DB 5; Length 373;
 Best Local Similarity 96.5%; Pred. No. 1.5e-64;
 Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

Qy	1	MEDLDQSP	LVSSSDSP	PRPQPA	FKYQFV	REP	EEEEEEEE	EEEEEEEE	DEDEDE	DEDEDE	LEE	LEV	L	R	K	P	A	60
Db	1	MEDLDQSP	LVSSSDSP	PRPQPA	FKYQFV	REP	EEEEEEEE	EEEEEEEE	DEDEDE	DEDEDE	LEE	LEV	L	R	K	P	A	60
Qy	61	AGLSA	APVPTA	PAAGAP	LMDFGN	DFVPP	APRG	PLPA	APPV	APER	QPSW	DPSP	VSST	V	P	A	P	120
Db	61	AGLSA	APVPTA	PAAGAP	LMDFGN	DFVPP	APRG	PLPA	APPV	APER	QPSW	DPSP	VSST	V	P	A	P	120
Qy	121	SPLS	AAVSP	SKLP	EDDE	PPAR	PPPP	PPAS	VSPQ	AE	PV	WT	PP	A	P	A	P	173
Db	121	SPLS	AAVSP	SKLP	EDDE	PPAR	PPPP	PPAS	VSPQ	AE	PV	WT	PP	A	P	A	P	180
Qy	174	-----	V	D	L	L	Y	W	R	D	I	K	K	T	G	V	F	228
Db	181	SSGS	V	V	D	L	L	Y	W	R	D	I	K	K	T	G	V	240
Qy	229	VIQAI	QKS	D	E	G	H	P	F	R	A	L	E	S	E	V	A	288
Db	241	VIQAI	QKS	D	E	G	H	P	F	R	A	L	E	S	E	V	A	300
Qy	289	KFAV	L	M	W	V	F	T	Y	V	G	A	L	F	N	G	L	348
Db	301	KFAV	L	M	W	V	F	T	Y	V	G	A	L	F	N	G	L	360
Qy	349	I	Q	A	K	I	P	G	L	K	R	K	A	E				

Db |||||
361 IQAKIPGLKRKAE 373

RESULT 8

ABG30937

ID ABG30937 standard; protein; 373 AA.

XX

AC ABG30937;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human NogoB protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
KW tissue hypertrophy; central nervous system; axon regeneration; NogoB;
KW Nogo-associated disease; metastasis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 92. .104

FT /note= "NogoB (ASY) peptide"

FT Peptide 180. .193

FT /note= "NogoB (ASY) peptide, distinguishes NogoB from
FT other Nogo isoforms"

FT Peptide 272. .285

FT /note= "NogoB (ASY) peptide"

XX

PN WO200257483-A2.

XX

PD 25-JUL-2002.

XX

PF 18-JAN-2002; 2002WO-GB000228.

XX

PR 18-JAN-2001; 2001GB-00001312.

XX

PA (GLAX) GLAXO GROUP LTD.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX

DR WPI; 2002-599722/64.

DR N-PSDB; ABK90133.

XX

PT Identifying modulators of Nogo or BACE activity for treating acute
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
PT providing and monitoring interaction between Nogo and BACE polypeptides.

XX

PS Example 1; Page 25; 68pp; English.

XX

CC The present invention relates to a new method of identifying modulators
CC of Nogo function or BACE activity. The method involves providing Nogo and
CC BACE polypeptides capable of binding with each other, monitoring the

interaction between these polypeptides, and determining if the test agent is a modulator of Nogo or BACE activity. The method is useful in treating acute neuronal injuries, such as spinal or head injury, stroke, peripheral nerve damage, and in neoplastic (e.g. glioblastomas, neuroblastomas), hyperproliferative or dysproliferative disorders (e.g. cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue hypertrophy) of the central nervous system. The BACE polypeptide is useful in screening methods to identify agents that may act as modulators of BACE activity and in particular agents that may be useful in treating Nogo-associated diseases. The modulators of Nogo or BACE polypeptides, and the polynucleotide encoding the BACE polypeptide are useful in manufacturing a medicament for the treatment or prevention of disorders responsive to the modulation of Nogo activity, in alleviating the symptoms or improving the condition of a patient suffering from this disorder, in axon regeneration, or in preventing metastasis or spreading of a cancer. The polynucleotide may also be an essential component in assays, a probe, in recombinant protein synthesis, and in gene therapy techniques. The present amino acid sequence represents the human NogoB protein of the invention

SQ Sequence 373 AA;

Query Match 98.7%; Score 1825.8; DB 5; Length 373;
Best Local Similarity 96.0%; Pred. No. 3e-64;
Matches 358; Conservative 1; Mismatches 2; Indels 12; Gaps 1;

Qy 1 MEDLDQSPVLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDSPVSSTVPAP 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 S P L S A A A V S P S K L P E D D E P P A R P P P P P A S V S P Q A E P V W T P P A P A P A A P P S T S ----- 173

Qy 174 -----VVDLLYWRDIKKTGVVFGLSLTIVFSIVSVTAYIALALLSVTISFRIYKG 228
 | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 229 VIQA IQSDEGHPFRAYLESEVAISEELV QKYSNSALGHVNCTIKELRRFLVDLDSL 288
| | | | |

Qy 289 KFAVLMWVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAK 348
| | | | | | | | | | | | | | | | | | | | | | | | |

Qy 349 IQAKIPGLKRKAE 361
| | | | | | | | | |

RESULT 9
AAY56967

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Query Match 95.0%; Score 1756.9; DB 3; Length 1192;
Best Local Similarity 30.3%; Pred. No. 1.3e-60;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

QY 1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
 |||
 Db 1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPNTISAGQEDFPSVLLETAASLPSLSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTKLVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDFSDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFISSKEAQIRETETFSDDSSPIEIIIDEFPTLISSKTDSSFKLAREYTDLEVSHKSEI	900
Qy	172	-----	171

Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDV SALAT 960
 Qy 172 -----TSVVDLLYWRDIKKTGVV 189
 Db 961 QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020
 Qy 190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE 249
 Db 1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE 1080
 Qy 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALENGLTL 309
 Db 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALENGLTL 1140
 Qy 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 Db 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 10

AAB82349

ID AAB82349 standard; protein; 1192 AA.

XX

AC AAB82349;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human NOGO-A protein.

XX

KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;
 KW cerebroprotective; neuroleptic; diagnosis; therapy.

XX

OS Homo sapiens.

XX

PN WO200136631-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-GB004345.

XX

PR 15-NOV-1999; 99GB-00026995.

PR 24-JAN-2000; 2000GB-00001550.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Michalovich D, Prinjha R;

XX

DR WPI; 2001-343822/36.

DR N-PSDB; AAF90324.

XX

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
 PT gene and may be useful in the treatment of neural disorders including
 PT Alzheimer's and Parkinson's diseases.

XX
PS Disclosure; Page 26-27; 25pp; English.

XX
CC The present sequence is that of human NOGO-A. NOGO-A is a previously
CC known splice variant of the human NOGO gene on chromosome 2p21. The
CC invention relates to a novel splice variant, NOGO-C (see AAB82348). It
CC provides NOGO-C polypeptides and polynucleotides, and methods for
CC producing such polypeptides by recombinant techniques. Also disclosed are
CC methods for utilising NOGO-C polypeptides and polynucleotides in the
CC treatment of diseases including neuropathies, spinal injury, brain
CC injury, stroke, neuronal degeneration, for example Alzheimer's disease
CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders
CC and developmental disorders. Also provided are methods for identifying
CC agonists and agonists for use in treating conditions associated with NOGO
CC -C imbalance, and diagnostic assays for detecting diseases associated
CC with inappropriate NOGO-C activity or levels

XX
SQ Sequence 1192 AA;

Query Match 95.0%; Score 1756.9; DB 4; Length 1192;
Best Local Similarity 30.3%; Pred. No. 1.3e-60;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171

Db	481	PLLGDP TSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSE	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQVPDPHSELVEDSSPDSEFVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEII DEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLLPPDV SALAT	960
Qy	172	-----TSVV D LLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVD LLYWRDIKKTGVV	1020
Qy	190	FGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 11

AAU04591

ID AAU04591 standard; protein; 1192 AA.

XX

AC AAU04591;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;
 KW cranial trauma; cerebral trauma; spinal cord injury; stroke;
 KW demyelinating disease; multiple sclerosis; monophasis demyelination;
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
 KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
 KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
 KW Canavan's disease; metachromatic leukodystrophy; viral infection;
 KW Krabbe's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1054. .1119
 FT /label= Lumenal_extracellular_domain
 FT /note= "This sequence is specifically claimed"
 FT Peptide 1055. .1094
 FT /label= Pep1
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1064. .1088
 FT /label= Pep2
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1074. .1098
 FT /label= Pep3
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1084. .1108
 FT /label= Pep4
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1095. .1119
 FT /label= Pep5
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 XX
 PN WO200151520-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001041.
 XX
 PR 12-JAN-2000; 2000US-0175707P.
 PR 26-MAY-2000; 2000US-0207366P.
 PR 29-SEP-2000; 2000US-0236378P.
 XX
 PA (UYYA) UNIV YALE.
 XX
 PI Strittmatter SM;
 XX
 DR WPI; 2001-442138/47.
 DR N-PSDB; AAS09453.
 XX
 PT Novel Nogo receptor protein useful for identifying modulator of Nogo
 PT protein or Nogo receptor protein, which is useful for treating central
 PT nervous system disorders.
 XX

PS Example 1; Page 101-104; 109pp; English.

XX

CC The sequence is the human Nogo protein, a 250kDa myelin-associated axon
CC growth inhibitor. The invention relates to the use of the nogo receptor,
CC nogo protein, their nucleic acids, vectors expressing them and antibodies
CC against them, to isolate agents which block nogo receptor mediated axonal
CC growth. The agent is useful for treating a central nervous system
CC disorder which is a result of cranial or cerebral trauma, spinal cord
CC injury, stroke or a demyelinating disease selected from multiple
CC sclerosis, monophasis demyelination, encephalomyelitis, multifocal
CC leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,
CC pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,
CC Spongy degeneration, Alexander's disease, Canavan's disease,
CC metachromatic leukodystrophy, viral infection and Krabbe's disease

XX

SQ Sequence 1192 AA;

Query Match 95.0%; Score 1756.9; DB 4; Length 1192;
Best Local Similarity 30.3%; Pred. No. 1.3e-60;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFVSVPKAEASAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540

Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQVPVDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETFSDDSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALENGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALENGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 12

ABG30938

ID ABG30938 standard; protein; 1192 AA.

XX

AC ABG30938;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human NogoA protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;
 KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;

KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
 KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;
 KW Nogo-associated disease; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN WO200257483-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 18-JAN-2002; 2002WO-GB000228.
 XX
 PR 18-JAN-2001; 2001GB-00001312.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
 XX
 DR WPI; 2002-599722/64.
 DR N-PSDB; ABK90134.
 XX
 PT Identifying modulators of Nogo or BACE activity for treating acute
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
 PT providing and monitoring interaction between Nogo and BACE polypeptides.
 XX
 PS Disclosure; Page 59-62; 68pp; English.
 XX
 CC The present invention relates to a new method of identifying modulators
 CC of Nogo function or BACE activity. The method involves providing Nogo and
 CC BACE polypeptides capable of binding with each other, monitoring the
 CC interaction between these polypeptides, and determining if the test agent
 CC is a modulator of Nogo or BACE activity. The method is useful in treating
 CC acute neuronal injuries, such as spinal or head injury, stroke,
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
 CC hypertrophy) of the central nervous system. The BACE polypeptide is
 CC useful in screening methods to identify agents that may act as modulators
 CC of BACE activity and in particular agents that may be useful in treating
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
 CC and the polynucleotide encoding the BACE polypeptide are useful in
 CC manufacturing a medicament for the treatment or prevention of disorders
 CC responsive to the modulation of Nogo activity, in alleviating the
 CC symptoms or improving the condition of a patient suffering from this
 CC disorder, in axon regeneration, or in preventing metastasis or spreading
 CC of a cancer. The polynucleotide may also be an essential component in
 CC assays, a probe, in recombinant protein synthesis, and in gene therapy
 CC techniques. The present amino acid sequence represents the human NogoA
 CC protein of the invention
 XX
 SQ Sequence 1192 AA;

Query Match 95.0%; Score 1756.9; DB 5; Length 1192;
 Best Local Similarity 30.3%; Pred. No. 1.3e-60;
 Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVLAQAQDSETDYVTTDNLTQVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQFACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLESITETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840

Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETETSDSSPIEIIDFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFETYVGALFNGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFETYVGALFNGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 13

ABP68600

ID ABP68600 standard; protein; 1192 AA.

XX

AC ABP68600;

XX

DT 14-JAN-2003 (first entry)

XX

DE Human pancreatic cancer expressed protein SEQ ID NO 71.

XX

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour.

XX

OS Homo sapiens.

XX

PN WO200260317-A2.

XX

PD 08-AUG-2002.

XX

PF 30-JAN-2002; 2002WO-US002781.

XX

PR 30-JAN-2001; 2001US-0265305P.

PR 31-JAN-2001; 2001US-0265682P.

PR 09-FEB-2001; 2001US-0267568P.

PR 21-MAR-2001; 2001US-0278651P.

PR 28-APR-2001; 2001US-0287112P.

PR 16-MAY-2001; 2001US-0291631P.

PR 12-JUL-2001; 2001US-0305484P.

PR 20-AUG-2001; 2001US-0313999P.

PR 27-NOV-2001; 2001US-0333626P.

XX

PA (CORI-) CORIXA CORP.

XX
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 XX
 DR WPI; 2002-627435/67.
 DR N-PSDB; ABV94680.
 XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic
 PT cancer.
 XX
 PS Claim 2; SEQ ID NO 71; 300pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
 CC complements of (a); (c) sequences consisting of at least 20 contiguous
 CC residues of (a); (d) sequences that hybridize to (a), under moderately
 CC stringent conditions; (e) sequences having at least 75% or 90% identity
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
 CC in a patient and compositions comprising polypeptides, polynucleotides,
 CC antibodies, fusion proteins, T cell populations and antigen presenting
 CC cells expressing the polypeptide are useful in treating pancreatic cancer
 CC and stimulating an immune response. The polynucleotides can be used as
 CC probes or primers for nucleic acid hybridisation, in the design and
 CC preparation of ribozyme molecules for inhibiting expression of the tumour
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene
 CC therapy. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1192 AA;

Query Match 95.0%; Score 1756.9; DB 5; Length 1192;
 Best Local Similarity 30.3%; Pred. No. 1.3e-60;
 Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171

Db	301	GSSFVSFSPAESAVIVANPREETIVKKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPTSENKTDEKKIEEKKQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETFSDDSPIEIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361

RESULT 14

ABB81078

ID ABB81078 standard; protein; 1192 AA.

XX

AC ABB81078;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; human; receptor.

XX

OS Homo sapiens.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86601.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in the
 PT central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides.

XX

PS Example; Page 53-56; 93pp; English.

XX

CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or

CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease is
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents the human
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
 CC antigen

XX

SQ Sequence 1192 AA;

Query Match 95.0%; Score 1756.9; DB 5; Length 1192;
 Best Local Similarity 30.3%; Pred. No. 1.3e-60;
 Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy	1	MEDLDQSPILVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPILVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTklVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171

Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETFSDDSPIELIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 15

ABR59667

ID ABR59667 standard; protein; 1192 AA.

XX

AC ABR59667;

XX

DT 22-JUL-2003 (first entry)
 XX
 DE Human NogoA protein.
 XX
 KW Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy;
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003031462-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 04-OCT-2002; 2002WO-US032007.
 XX
 PR 06-OCT-2001; 2001US-00972599.
 XX
 PA (UYYA) UNIV YALE.
 XX
 PI Strittmatter SM;
 XX
 DR WPI; 2003-393433/37.
 DR N-PSDB; ACC81048.
 XX
 PT New human Nogo receptor polypeptides and nucleic acids, useful for
 PT decreasing inhibition of axonal growth by a central nervous system
 PT neuron, or in treating central nervous system disease, disorder or
 PT injury, e.g. spinal cord injury.
 XX
 PS Disclosure; Page 131-135; 148pp; English.
 XX
 CC The invention relates to a novel nucleic acid encoding a polypeptide
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
 CC human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of P1 with
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS
 CC domain, provided that a partial CTS domain, if present, consists of no
 CC more than the first 39 consecutive residues. The nucleic acid of the
 CC invention has neuroprotective activity. The polynucleotide may have a use
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
 CC axonal growth by a central nervous system (CNS) neuron. The NgR
 CC polypeptide or an agent inhibits the binding of Nogo to NgR or NgR-
 CC dependent signal transduction in the central nervous system neuron may be
 CC used in treating central nervous system disease, disorder or injury, e.g.
 CC spinal cord injury. Expression of an NgR protein may be associated with
 CC inhibition of axonal regeneration following cranial, cerebral or spinal
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
 CC monophasic demyelination, encephalomyelitis, multifocal
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
 CC sequence is used in the exemplification of the invention
 XX
 SQ Sequence 1192 AA;

Query Match 95.0%; Score 1756.9; DB 6; Length 1192;
 Best Local Similarity 30.3%; Pred. No. 1.3e-60;

Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFVSVPKAEASAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPTSENKTDEKKIEEKKAIQVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840

Qy	172	-----	171
Db	841	SNDDLFISKEAQIRETETFSDDSSPIEIIDFPTLISSKTDsFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSALAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVAVLMWVFTYVGALENGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVAVLMWVFTYVGALENGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

Search completed: September 29, 2004, 18:51:25
Job time : 97.6283 secs

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:48:38 ; Search time 23.5326 Seconds
(without alignments)
791.964 Million cell updates/sec

Title: SEQ29_1-172_990-1178
Perfect score: 1850
Sequence: 1 MEDLDQSPLVSSSDSPPRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	927	50.1	199	2	US-08-700-607-1	Sequence 1, Appli
2	827.7	44.7	776	2	US-08-700-607-5	Sequence 5, Appli
3	789.8	42.7	356	2	US-08-700-607-6	Sequence 6, Appli
4	684.2	37.0	208	2	US-08-700-607-7	Sequence 7, Appli
5	666	36.0	267	2	US-08-700-607-8	Sequence 8, Appli
6	541.9	29.3	168	4	US-09-149-476-563	Sequence 563, App
7	538.3	29.1	241	2	US-08-700-607-3	Sequence 3, Appli
8	348.9	18.9	75	4	US-09-621-976-4600	Sequence 4600, Ap
9	348.9	18.9	75	4	US-09-621-976-4601	Sequence 4601, Ap
10	285	15.4	92	4	US-09-149-476-411	Sequence 411, App
11	259.7	14.0	1248	2	US-09-080-897-2	Sequence 2, Appli

12	259.7	14.0	1248	3	US-09-323-735-2	Sequence 2, Appli
13	258.2	14.0	1315	3	US-08-899-595-3	Sequence 3, Appli
14	256.5	13.9	1255	2	US-09-080-897-4	Sequence 4, Appli
15	256.5	13.9	1255	3	US-08-899-595-1	Sequence 1, Appli
16	256.5	13.9	1255	3	US-09-323-735-4	Sequence 4, Appli
17	246.1	13.3	8991	4	US-08-714-741-32	Sequence 32, Appl
18	245.8	13.3	1070	3	US-08-922-635-22	Sequence 22, Appl
19	245.8	13.3	1504	4	US-09-364-206-2	Sequence 2, Appli
20	243.6	13.2	1719	2	US-08-459-568-4	Sequence 4, Appli
21	243.6	13.2	1719	2	US-08-399-411-4	Sequence 4, Appli
22	243.6	13.2	1719	3	US-08-516-859A-4	Sequence 4, Appli
23	243.6	13.2	1719	4	US-09-586-472-4	Sequence 4, Appli
24	243.6	13.2	1719	4	US-09-528-706-4	Sequence 4, Appli
25	241.5	13.1	933	3	US-08-764-870-14	Sequence 14, Appl
26	241.5	13.1	933	3	US-08-980-115-14	Sequence 14, Appl
27	238.7	12.9	1706	2	US-08-459-568-2	Sequence 2, Appli
28	238.7	12.9	1706	2	US-08-399-411-2	Sequence 2, Appli
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30	238.7	12.9	1706	4	US-09-586-472-2	Sequence 2, Appli
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32	234.1	12.7	1326	4	US-09-688-188B-15	Sequence 15, Appl
33	234.1	12.7	1326	4	US-09-291-417D-15	Sequence 15, Appl
34	223.9	12.1	1266	4	US-08-506-296B-4	Sequence 4, Appli
35	223.9	12.1	2972	4	US-09-579-181-2	Sequence 2, Appli
36	223.9	12.1	3118	4	US-09-579-181-1	Sequence 1, Appli
37	223.4	12.1	1665	4	US-09-858-664A-2	Sequence 2, Appli
38	223.4	12.1	1665	4	US-10-274-978-2	Sequence 2, Appli
39	223.3	12.1	1274	4	US-09-095-443-2	Sequence 2, Appli
40	221.9	12.0	1601	4	US-09-345-473E-40	Sequence 40, Appl
41	221.7	12.0	559	4	US-10-116-370-2	Sequence 2, Appli
42	220.8	11.9	1185	3	US-09-041-886-23	Sequence 23, Appl
43	220.5	11.9	2205	1	US-08-093-453B-2	Sequence 2, Appli
44	219.2	11.8	905	2	US-08-574-959A-9	Sequence 9, Appli
45	219.2	11.8	905	3	US-09-357-014-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304


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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-1

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Query Match          50.1%; Score 927; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 5.7e-34;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 71

Qy      234 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 293
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Db      72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 131

Qy      294 MWVFTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 353
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Db      132 MWVFTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy      354 PGLKRKAE 361
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Db      192 PGLKRKAE 199

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RESULT 2

US-08-700-607-5

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; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.

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; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

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Query Match          44.7%; Score 827.7; DB 2; Length 776;
Best Local Similarity 27.1%; Pred. No. 2e-28;
Matches 196; Conservative 55; Mismatches 89; Indels 383; Gaps 17;

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Qy      10 ----VSSSDSPPR---PQP----- 21
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Db      130 ENGHVTISESPEELGTPGSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQM 189

Qy      22 ---AFKYQFVREPEDEEEEEEEEEDEDEDLE----- 50
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Db      190 KAEAYKYIDITRPEEVKHHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDKPAPVEGKI 249

Qy      51 -----ELE----- 53
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Qy      54 -----VLERKPAAGLS-- 64

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Qy      65 ----AAPV-----PTAPAAAGAPL----- 78
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Qy      79 -----MDFGNDFVPPAPRGPLPAAPPV-----APE 103
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Db      427 LPSGYVSFGHVGGPP----PSPASPSIQYSILREEREAEELDSELIIESCDASSASEESPK 482
Qy      104 RQ---PSWDPSPVS-----STVPAPSPLSAAAVSP 130
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Db      483 REQDSPPMKPSALDAIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGP----- 534
Qy      131 SKLPEDD-----EPPARPPPPPPASVSPQAEPVWTPPAP-APAAPP-----STSVVDLL 178
      : | | | | | | | | | | : | | | | | : | | |
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Qy      179 YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDE 238
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Qy      239 GHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFT 298
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Db      654 GHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLQELRRLFLVQDLVDLSLKFAVLMWLLT 713
Qy      299 YVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKR 358
      | | | | | | | | | | : : : : : : : : : : : : | | | | | | | | | | : : : | | | | | | | |
Db      714 YVGALFNGLTLLLMVAVSMFTLPVVVYVKHQAQIDQYLGIVRTHINAVVAKIQAKIPGAKR 773
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Db      774 HAE 776

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RESULT 3

US-08-700-607-6

; Sequence 6, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

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;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/700,607
;   FILING DATE:  Filed Herewith
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Billings, Lucy J.
;   REGISTRATION NUMBER:  36,749
;   REFERENCE/DOCKET NUMBER:  PF-0114 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-855-0555
;   TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  356 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   IMMEDIATE SOURCE:
;   LIBRARY:  GenBank
;   CLONE:  307309
US-08-700-607-6

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Best Local Similarity 42.6%;  Pred. No. 2.2e-27;
Matches 169;  Conservative 42;  Mismatches 74;  Indels 112;  Gaps 10;

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Qy      59 PAAGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP-----E 103
      :||: | |
Db      67 -----SPPMKPSALDAIREETGVRAEE 88

Qy     104 RQPS----WDPS---PVSSTVPAPSPLSAAAVSPSKLPEDD-----EPPARPPPPPPASV 151
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Db      89 RAPSRRGLAEPGSFLDYPSTEPQPGP-----ELPPGDGALEPETPMLPRKPEEDSS 139

Qy     152 SPQAEFVWTPPAP-APAAPP-----STSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS 204
      | |: | | || | :|||||||:|:| |: | | || |
Db     140 SNQSPAATKGPGPLGPGAPPLLFLNKQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFS 199

Qy     205 IVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEELVQKYSNSA 264
      :||| ||:| || ||||| | :||:|:| |||||:| || | : :| :|||:
Db     200 VVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTDCL 259

Qy     265 LGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIY 324
      :|| |:||||||| ||||| : ||||| :|:|:|:|:|:|:|
Db     260 QFYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLLMVAVSMFTLPVVY 319

Qy     325 ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
      :|||| | ||| : : ||||| || ||
Db     320 VKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 356

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US-08-700-607-7

US-08-700-607-7

Qy	152	SPQAEPVWTPPAPAPAAPPSTSVVDLLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAY	211
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Db	7	STKMDCVW-----SNWKSQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAY	58
Qy	212	IALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCT	271
		: : : : : : : : : :	
Db	59	LALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQIKYTDCLQFYVNST	118

Qy 272 IKELRRRLFLVDDLVDLSLKFAVLMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQI 331
 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 Db 119 LKELRRRLFLVQDLVDLSLKFAVLMWLLTYVGALENGLTLLIMAVVSMFTLPVVYVKHQAQI 178
 Qy 332 DHYLG LANKNVKDAMAKIQAKIPGLKRKAE 361
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 Db 179 DQYLG LVRTHINAVVAKIQAKIPGAKRHAE 208

RESULT 5

US-08-700-607-8

; Sequence 8, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 267 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 281046

US-08-700-607-8

Query Match 36.0%; Score 666; DB 2; Length 267;

Best Local Similarity 66.1%; Pred. No. 4e-22;

Matches 123; Conservative 34; Mismatches 29; Indels 0; Gaps 0;

Qy 172 TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 231
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Db 10 SQAIDLLYWRDIKQTGIVFGSFLLLSLTQFSVSVVAYLALAALSATISFRIYKSVLQ 69

Qy 232 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFA 291
|:|:|:|:|:|:| | | | | | :|:|:| :|:|:| :| | | | | | | | | | |
Db 70 AVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQLYVNSTLKELRRLFLVQDLVDLSLKFA 129

Qy 292 VLMWVFTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA 351
| | | | : | | | | | | | | | | :|:|:|:|:|:|:| | :| | | | | | | | :| | | | |
Db 130 VLMWLLTYVGALFENGLTLLMAVVSMTLPVVYVKHQAQVDQYLGLVTRTHINTVVAKIQA 189

Qy 352 KIPGLK 357
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Db 190 KIPGAR 195

RESULT 6

US-09-149-476-563

; Sequence 563, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,502

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,633

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,583

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,617

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
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; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
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; EARLIER APPLICATION NUMBER: 60/047,632
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; EARLIER APPLICATION NUMBER: 60/047,601
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; EARLIER APPLICATION NUMBER: 60/043,580
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; EARLIER APPLICATION NUMBER: 60/043,568
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; EARLIER APPLICATION NUMBER: 60/043,314
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; EARLIER APPLICATION NUMBER: 60/043,311
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; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586

Qy 256 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSIKFAVLMWVFTYVGALENGLTLLILALI 315
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 Db 61 AFHNYMNAAMVHINRALKLIIRLFLVEDLVDLSLKLAVFMWLMTYVGAENGITLLILAE 120
 Qy 316 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 361
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 Db 121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE 167

RESULT 7

US-08-700-607-3

; Sequence 3, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 241 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY: THP1NOB01

; CLONE: 31870

US-08-700-607-3

Query Match 29.1%; Score 538.3; DB 2; Length 241;
 Best Local Similarity 30.9%; Pred. No. 1.6e-16;

Matches 112; Conservative 38; Mismatches 46; Indels 167; Gaps 4;

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Qy     66 APVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVPAPSPLSA 125
      |:|| |
Db     19 GAEPSAPGGGG-----29

Qy    126 AAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPP-----STSVVD 176
                        :| | | | :| |
Db     30 -----SPGACPALGTKSCSSSCAVHD 50

Qy    177 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKS 236
      |: |||:|||| ||| :| :|||| ||: ||| :| : ||||| ||||| |||: |||
Db     51 LIXWRDVKKTGFVFGTTLIMLLSLAASFVISVVSYLILALLSVTISFRIYKSVIQAVQKS 110

Qy    237 DEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWV 296
      :|||||:||||: :: :| | | :|: | :| : | : |||||:|||||| || ||:
Db    111 EEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRAKLIIRLFLVEDLVDLSLKLAFFMWL 170

Qy    297 FTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL 356
      |||||:||||:||||| : : |||: || : : | : || |
Db    171 MTYVGAVFNGITLLILAELLIXSVPIVYXKY-----KVPSKTPWN 210

Qy    357 KRK 359
      ::|
Db    211 RQK 213
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RESULT 8

US-09-621-976-4600

; Sequence 4600, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 4600

; LENGTH: 75

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: 58

; OTHER INFORMATION: Xaa = His,Pro

; NAME/KEY: UNSURE

; LOCATION: 28

; OTHER INFORMATION: Xaa = Met,Val

; NAME/KEY: UNSURE

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; LOCATION: 19
; OTHER INFORMATION: Xaa = Pro,Gln
; NAME/KEY: UNSURE
; LOCATION: 53
; OTHER INFORMATION: Xaa = Ser,Tyr
US-09-621-976-4600
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Query Match 18.9%; Score 348.9; DB 4; Length 75;
Best Local Similarity 82.6%; Pred. No. 4.4e-09;
Matches 71; Conservative 0; Mismatches 4; Indels 11; Gaps 1;

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Db      1 MEDLDQSPLVSSSDSPPRXQPAFKYQFXREPEDEE-----EDLEELEVLERKPA 49
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Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFV 86
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Db     50 AGLXAAPVXTAPAAGAPLMDFGNDFV 75

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RESULT 9
US-09-621-976-4601
; Sequence 4601, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4601
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 58
; OTHER INFORMATION: Xaa = His,Pro
; NAME/KEY: UNSURE
; LOCATION: 28
; OTHER INFORMATION: Xaa = Met,Val
; NAME/KEY: UNSURE
; LOCATION: 19
; OTHER INFORMATION: Xaa = Pro,Gln
; NAME/KEY: UNSURE
; LOCATION: 53
; OTHER INFORMATION: Xaa = Ser,Tyr
US-09-621-976-4601

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Query Match 18.9%; Score 348.9; DB 4; Length 75;
Best Local Similarity 82.6%; Pred. No. 4.4e-09;
Matches 71; Conservative 0; Mismatches 4; Indels 11; Gaps 1;

; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
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; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
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; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23

Query Match 15.4%; Score 285; DB 4; Length 92;
Best Local Similarity 57.1%; Pred. No. 4.5e-06;
Matches 52; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

RESULT 11
US-09-080-897-2
; Sequence 2, Application US/09080897

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; Patent No. 5985574
; GENERAL INFORMATION:
; APPLICANT: King, Mary-Claire
; APPLICANT: Lynch, Eric D.
; APPLICANT: Lee, Ming
; APPLICANT: Morrow, Jan E.
; APPLICANT: Welcsh, Piri L.
; APPLICANT: Leon, Pedro E.
; TITLE OF INVENTION: Modulators of Actin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UW97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-080-897-2

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Query Match          14.0%; Score 259.7; DB 2; Length 1248;
Best Local Similarity 15.6%; Pred. No. 0.0088;
Matches 143; Conservative 49; Mismatches 114; Indels 613; Gaps 40;

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Db      378 MDDFNEVFQILLNTVKDSKAEPHFLSILQHLLLVRNDYEARPQYYKLIEECISQIVLHKN 437

Qy      21 ---PAF----- 23
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Db      438 GADPDFKCRHLQIEIEGLIDQMIDKTKVEKSEAKAAELEKKLDSELTARHELQVEMKKME 497

Qy      24 -----KYQFVREPEDEEEEEEEEEDEDEDLE-----ELEVLERKPAAGL 63
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Qy 64 SA-----APVPTA-----PAAGAPLMDFGNDVPPAPRGPLPAAPP- 99
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Qy 100 -----VAPERQPSWDSPVS--STVPAPSPL--SAAAVSPSKLPE----DDEPP---AR 142
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 Db 613 PGGTAISP-----PPPLSGDATIPPPPLPEGVGIPSPSSLPGGTAIPPPPPPLPGSAR 665

Qy 143 -PPPPPP--ASVSPQAEPV-----WTPPAPAPAAP----- 169
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 Db 666 IPPPPPPPLPGSAGIPPPPPPLPGEAGMPPPPPPPLPGGPGIPPPPPFPGGPGIPPPPPGMG 725

Qy 170 -----PSTSVV-----DL---LYWRDIK---- 184
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Qy 185 -----KT----- 186
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 Db 786 ENNELFAKLTLTFSAQTKTKKDQEGGEEKKSVQKKVKELKVLDSKTAQNLSIFLGSFRM 845

Qy 187 -----GVVFG- 191
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 Db 846 PYQEIKNVILEVNEAVLTESMIQNLIKQMPPEPEQLKMLSELKDEYDDLAESEQFGVVMGT 905

Qy 192 -----ASLFLLLSLTVFS-----IVSVTAYIALA-----LLSVTI 221
 | || | || |||| | || :|
 Db 906 VPRLRPRLNAILFKL----QFSEQVENIKPEIVSVTA----ACEELRKSESFSNLEITL 957

Qy 222 -----SFRI-----YKGVIQAIQKS 236
 | | | :|
 Db 958 LVGNMAGSRNAGAFGNISFLCKLRDTKSTDQKMTLLHFLAELCENDYPDVLKF---P 1014

Qy 237 DEGHPPFRAYLESEVAISEELVQK----- 259
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 Db 1015 DE----LAHVEKASRVSAENLQKNLDQMKKQISDVERDVQNFPAATDEKDKFVEKMTSEV 1070

Qy 260 -----YSNSALGHVN--CTIKEL-----RRLEFL----- 280
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Qy 281 -----VDDLVDLSLKFAVLMWV 296
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 Db 1131 RRKTEEKMRRAKLAKAEKERLEKQQKREQLIDMNAEGDETGVMDSLLEALQ----- 1183

Qy 297 FTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLG-----LANKNVK--DAMAKI 349
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 Db 1184 ---SGAAFR-----RKRGPQANRKAGCAVTSLLASELTKDDAMAAV 1222

Qy 350 QAKI-----PGLKRKAE 361
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 Db 1223 PAKVSKNSETFPTILEEAK 1241

RESULT 12

US-09-323-735-2

; Sequence 2, Application US/09323735

; Patent No. 6197932

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; GENERAL INFORMATION:
; APPLICANT: King, Mary-Claire
; APPLICANT: Lynch, Eric D.
; APPLICANT: Lee, Ming
; APPLICANT: Morrow, Jan E.
; APPLICANT: Welcsh, Piri L.
; APPLICANT: Leon, Pedro E.
; TITLE OF INVENTION: Modulators of Actin
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/323,735
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/080,897
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UW97-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-323-735-2

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Query Match          14.0%; Score 259.7; DB 3; Length 1248;
Best Local Similarity 15.6%; Pred. No. 0.0088;
Matches 143; Conservative 49; Mismatches 114; Indels 613; Gaps 40;

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Qy      21 ---PAF----- 23
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Db      438 GADPDFKCRHLQIEIEGLIDQMIDKTKVEKSEAKAAELEKKLDSELTARHELQVEMKKME 497

Qy      24 -----KYQFVREPEDEEEEEEEEEDEDEDLE-----ELEVLERKPAAGL 63
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Db 498 SDFEQLQDLQGEKDALHSEKQQIATEKQDLEAEVSQLTGEVAKLTKELED-AKKEMASL 556

Qy 64 SA-----APVPTA-----PAAGAPLMDFGNDFVPPAPRGPLPAAPP- 99
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Db 557 SAAAITVPPSVPSRAPVPPAPPLPGDSGTIIPPPAP---GDSTTPPPPPPPPPPPPL 612

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Db 613 PGGTAISP-----PPPLSGDATIPPPPLPEGVGIPSPSSLPGGTAIPPPPLPGSAR 665

Qy 143 -PPPPPP---ASVSPQAEPV-----WTPPAPAPAAP----- 169
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Db 666 IPPPPPLPGSAGIPPPPLPGEAGMPPPPPLPGGPGIPPPPPFGGPGIPPPPPGMG 725

Qy 170 -----PSTSVV-----DL---LYWRDIK---- 184
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Db 726 MPPPPPFPGFVPAAPVLPFGLTPKKLYKPEVQLRRPNWSKLVAEDLSQDCFWTQVKEDRF 785

Qy 185 -----KT----- 186
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Db 786 ENNELFAKLTLTFSAQTKTKKDQEGGEEKKSVQKKVKELKVLDSKTAQNLSIFLGSFRM 845

Qy 187 -----GVVFG- 191
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Db 846 PYQEIKNVILEVNEAVLTESMIQNLIKQMPPEPEQLKMLSELKDEYDDLAESEQFGVVMGT 905

Qy 192 -----ASLFLLLSLTVFS-----IVSVTAYIALA-----LLSVTI 221
 | | | | | | | | | | | | |

Db 906 VPRLRPRLNAILFKL---QFSEQVENIKPEIVSVTA---ACEELRKSESFSNLEITL 957

Qy 222 -----SFRI-----YKGVIAIQKS 236
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Db 958 LVGNMAGSRNAGAFGFNISFLCKLRDTKSTDQKMTLLHFLAELCENDYPDVLFK---P 1014

Qy 237 DEGHPFRAYLESEVAISEELVQK----- 259
 || | : | : | | : |

Db 1015 DE----LAHVEKASRVSANLQKNLDQMKKQISDVERDVQNFPAAATDEKDKFVEKMTSFV 1070

Qy 260 -----YSNSALGHVN--CTIKEL-----RRLFL----- 280
 | : : | | | | | : |

Db 1071 KDAQEQYNKLMMHSNMETLYKELGEYFLFDPKKLSVEEFFMDLHNFRNMFLQAVKENQK 1130

Qy 281 -----VDDLVDSLKFAVLMWV 296
 : | | : : |

Db 1131 RRKTEEKMRRAKLAKEKAERLEKQKREQLIDMNAEGDETGVMDSLLEALQ----- 1183

Qy 297 FTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG-----LANKNVK-DAMAKI 349
 || | : | : | | : | | | |

Db 1184 ---SGAAFR-----RKRGPQANRKAGCAVTSLLASELTKDDAMAAV 1222

Qy 350 QAKI-----PGLKRKAE 361
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Db 1223 PAKVSKNSETFPTILEEAK 1241

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; Sequence 3, Application US/08899595
; Patent No. 6111072
; GENERAL INFORMATION:
;   APPLICANT: Narumiya, Shuh
;   APPLICANT: Takahashi, No. 6111072uaki
;   TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
;   TITLE OF INVENTION: ENCODING SAME
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 3000 K Street, N.W., Suite 500
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20007-5109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/899,595
;     FILING DATE: 24-JUL-1997
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: JP 8-242701
;     FILING DATE: 26-AUG-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: JP 9-90170
;     FILING DATE: 25-MAR-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Stephen A. Bent
;     REGISTRATION NUMBER: 29,768
;     REFERENCE/DOCKET NUMBER: 049441/0112
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202)672-5300
;     TELEFAX: (202)672-5399
;     TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1315 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-899-595-3

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Query Match          14.0%; Score 258.2; DB 3; Length 1315;
Best Local Similarity 15.3%; Pred. No. 0.011;
Matches 143; Conservative 49; Mismatches 114; Indels 628; Gaps 40;

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Qy      1 MEDLD-----QSPLVSSSDSPPRPQ----- 20
      |:| :           | |: :|   |||
Db      430 MDDFNEVFQILLNTVKDSKAEPHFLSLQHLLLVVRNDYEARPQYYKLIEECISQIVLHKN 489

Qy      21 ---PAF----- 23
      | |
Db      490 GADPDFKCRHLQIEIEGLIDQMIDKTKVEKSEAKAAELEKKLDSELTARHELQVEMKKME 549

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Qy 24 -----KYQFVREPEDEEEEEEEEEDEDEDELE-----ELEVLERKPAAGL 63
 | | :: :| |:: | :|| | | :| | |
 Db 550 SDFEQKLQDLQGEKDALHSEKQQIATEKQDLEAEVSQLTGEVAKLTKELED-AKKEMASL 608
 Qy 64 SA-----APVPTA-----PAAGAPLMDFGNDVFVPPAPRGPLPAAPP- 99
 || ||| | | | : | | | | | |
 Db 609 SAAAITVPPSVPSRAPVPPAPPLPGDSGTIIPPPAP----GDSTTPPPPPPPPPPPPL 664
 Qy 100 -----VAPERQPSWDPSVVS--STVPAPSPL--SAAAVSPSKLPEDDE 138
 ::| | :| :| | | | | | |
 Db 665 PGGVCISSPPSLPGGTAISP-----PPPLSGDATIPPPPLPEGVGIPSPSSPLPGGTA 717
 Qy 139 ----PP----AR-PPPPPP--ASVSPQAEV-----WTPPAPAPA 167
 || || |||| | : | : | | | |
 Db 718 IPPPPPLPGSARIPPPPPPLPGSAGIPPPPPPLPGEAGMPPPPPLPGGPGIPPPPPFPG 777
 Qy 168 AP-----PSTSVV-----DL-- 177
 | | : | : | | |
 Db 778 GPGIPPPPPGMGMPPPPPFPGFVPAAPVLPFGLTPKKLYKPEVQLRRPNWSKLVAEDLSQ 837
 Qy 178 -LYWRDIK----- 184
 :| :|
 Db 838 DCFWTKVKEDRFENNELFAKLTLTFSAQTKTSKAKKDQEGGEEKSVQKKVKELKVLDS 897
 Qy 185 KT----- 186
 ||
 Db 898 KTAQNLSIFLGSFRMPYQEIKNVILEVNEAVLTESMIQNLIKQMPPEPEQLKMLSELKDEY 957
 Qy 187 -----GVVFG-----ASLFLLLSLTVFS-----IVSVTAYIALA--- 215
 ||| | | | | | | | |
 Db 958 DDLAESEQFGVVMGTVPRLRPRLNAILFKL---QFSEQVENIKPEIVSVTA---ACEE 1009
 Qy 216 -----LLSVTI-----SFRI----- 225
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 Db 1010 LRKSESFSNLLLEITLLVGNMAGSRNAGAFGFNISFLCKLRDTKSTDQKMTLLHFLAEL 1069
 Qy 226 ----YKGVIAIQKSDEGHPFRAYLESEVAISEELVQK----- 259
 | | :| || | :| :| | :| |
 Db 1070 CENDYPDVLKF---PDE---LAHVEKASRVSAENLQKNLDQMKKQISDVERDVQNFPAA 1122
 Qy 260 -----YSNSALGHVN--CTIKEL----- 275
 | : : | | | |
 Db 1123 TDEKDKFVEKMTSFVKDAQEQYNKLMMHSNMETLYKELGEYFLFDPKKLSVEEFFMDLH 1182
 Qy 276 --RRLFL-----V 281
 | :|| :
 Db 1183 NFRNMFLQAVKENQKRRETEEKMRRAKLAKEKAERLEKQQKREQLIDMNAEGDETGVM 1242
 Qy 282 DDLVDSLKFAVLMWVFYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLG----- 336
 | | :| :| | | : | : |
 Db 1243 DSLLEALQ-----SGAAFR-----RKRGRQANRKAGCAVTS 1274
 Qy 337 -LANKNVK-DAMAKIQAKI-----PGLKRKAE 361
 || :| |||| : || : | : :| :
 Db 1275 LLASELTKDDAMAAPPAKVSKNSETFPTILEEAK 1308

RESULT 14
 US-09-080-897-4
 ; Sequence 4, Application US/09080897
 ; Patent No. 5985574
 ; GENERAL INFORMATION:
 ; APPLICANT: King, Mary-Claire
 ; APPLICANT: Lynch, Eric D.
 ; APPLICANT: Lee, Ming
 ; APPLICANT: Morrow, Jan E.
 ; APPLICANT: Welcsh, Piri L.
 ; APPLICANT: Leon, Pedro E.
 ; TITLE OF INVENTION: Modulators of Actin
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 75 DENISE DRIVE
 ; CITY: HILLSBOROUGH
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94010
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/080,897
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: UW97-001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 343-4341
 ; TELEFAX: (650) 343-4342
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1255 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-080-897-4

Query Match 13.9%; Score 256.5; DB 2; Length 1255;
 Best Local Similarity 14.7%; Pred. No. 0.012;
 Matches 130; Conservative 42; Mismatches 135; Indels 575; Gaps 31;

QY	6	QSPLVSSSDSPPRPQ-----PAF-----	23
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Db	406	QHLLLVVRNDYEARPQYYKLIEECVSQIVLHKNGTDPDFKCRHLQIDIERLVDQMIDKTKV	465
QY	24	-----KYQFVREP	31
		:	
Db	466	EKSEAKATELEKKLDSELTARHELQVEMKKMENDFEQKLQDLQGEKDALDSEKQQITAQK	525

Qy	32	EDEEEEE-----EEEEDEDEDLEEEVLERKPAAGLSAAPVPTAPAAGAPIMDF	81
		: : : : :	
Db	526	QDLEAEVSKLTGEVAKLSKELEDAKNEMASLSAVVAPSVSSSAVPPAPPLPG----	DS 581
Qy	82	GNDFVPPAPRGPLPA-----APPVAP-----	102
		:	
Db	582	GTVIPPPPPPPPLPGGVPPSPPLPPGTCIPPPPPPLPGGACIPPPQPLPGSAAIPPPPL	641
Qy	103	---ERQPSWDPSPVSSSTVPAPSPLSAAVSPSKLPEDDEPPARP-----	143
		:	
Db	642	PGVASIPPPPPPLPGATAIPPPPPPLPGATAIP-----PPPPLPGGTGIPPPPPPLPGSV	694
Qy	144	--PPPPPASVSPQAEVWTPPAPAPAAP-----PSTSVV-----	175
		: :	
Db	695	GVPPPPPLPGGPGGLPP---PPPPFPGAPGIPPPPPGMGVPPPPFPGFVPAAPVLPFGLT	751
Qy	176	-----DL---LYWRDIK-----	184
		: :	
Db	752	PKKVYKPEVQLRRPNWSKFVAEDLSQDCFWTKVKEDRFENNELFAKLTIAFSAQTKT SKA	811
Qy	185	-----KT-----	186
Db	812	KKDQEGGEEKSVQKKVKELKVLD SKTAQNLSIFLGSRMPYQEIKNVILEVNEAVLTE	871
Qy	187	-----GVVFG-----ASLFLLLSLT	201
Db	872	SMIQNLIKQMPPEPEQLKMLSELKEEYDDLAESEQFGVVMGTVPRLRPNAILFKL----	927
Qy	202	VFS-----IVSVTA-----YIALALL-----SVTISF-	223
		:	
Db	928	QFSEQVENIKPEIVSVTAACEELRKSENFSSILLELTLLVGNMAGSRNAGAFGFNISFL	987
Qy	224	---RIYKGVIQAI-----QKSDEGHP-----FRAYLESEVAISEELVQK-----	259
		: : : : : :	
Db	988	CKLRDTKSADQKMTLLHFLAELCENDHPEVLKFPDELAHVEKASRVSAENLQKSLDQMKK	1047
Qy	260	-----YSNSALGHVN--CTIKEL-----	275
		: :	
Db	1048	QIADVERDVQNFPAAATDEKDKFVEKMTSFVKDAQEQYNKLMMHSNMETLYKELGDYFVF	1107
Qy	276	-----RRLFL-----	280
		:	
Db	1108	DPKKLSVEEFFMDLHNFRNMFQAVKENQKRRETEEKMRRAKLAKAEKERLEKQQKRE	1167
Qy	281	-----VDDLVDSLKFVILMWVFTYVGFALFNGLTLLILALISLFSVPVIYER	326
		: : : : :	
Db	1168	QLIDMNAEGDETGVMDSLLEALQ-----SGAAFR-----RKR	1199
Qy	327	HQAQIDHYLG-----LANKNVK-DAMAKIQAKIPGLKRKAE	361
		: : : : :	
Db	1200	GPRQVNRKAGCAVTSLLASELTKDDAMAPGPVKVP---KKSE	1238

RESULT 15
 US-08-899-595-1
 ; Sequence 1, Application US/08899595

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; Patent No. 6111072
; GENERAL INFORMATION:
; APPLICANT: Narumiya, Shuh
; APPLICANT: Takahashi, No. 6111072uaki
; TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,595
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-242701
; FILING DATE: 26-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 9-90170
; FILING DATE: 25-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Stephen A. Bent
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 049441/0112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-595-1

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Query Match          13.9%; Score 256.5; DB 3; Length 1255;
Best Local Similarity 14.7%; Pred. No. 0.012;
Matches 130; Conservative 42; Mismatches 135; Indels 575; Gaps 31;

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Qy          6 QSPLVSSSDSPPRPQ-----PAF----- 23
              | |: :| |||                      | |
Db          406 QHLLLVVRNDYEARPQYYKLIEECVSQIVLHKNGTDPDFKCRHLQIDIERLVDQMIDKTKV 465

Qy          24 -----KYQFVREP 31
                                   | | :
Db          466 EKSEAKATELEKKLDSELTARHELQVEMKKMENDFEQKLQDLQGEKDALDSEKQQITAQK 525

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Qy 32 EDEEEEE-----EEEEDEDEDLEELVLERKPAAGLSAAPVPTAPAAAGAPLMDF 81
 :| | | :| | | :| :| :| | | | | | |
 Db 526 QDLEAEVSKLTGEVAKLSKELEDANKEMASLSAVVVAHSVSSAAVPPAPPLPG----DS 581

Qy 82 GNDFVPPAPRGPLPA-----APPVAP----- 102
 | | | | | :| | :|
 Db 582 GTVIPPPPPPPPLPGGVVPPSPPLPPGTCIPPPPPPLPGGACIPPPPPQLPGSAAIPPPPPPL 641

Qy 103 ---ERQPSWDPSFVSSTVPAPSPLSAAAVSPSKLPEDDEPPARP----- 143
 | | | :| :| | | | | | | | |
 Db 642 PGVASIPPPPPPLPGATAIPPPPPPLPGATAIP-----PPPPPLPGGTGIPPPPPPLPGSV 694

Qy 144 --PPPPASVSPQAEPVWTPAPAPAAP-----PSTSVV----- 175
 | | | | | | | | | | | | | | :| :|
 Db 695 GVPPPPPLPGGPGGLPP---PPPPFPGAPGIPPPPPGMGVPPPPPFGFGVPAAPVLPFGLT 751

Qy 176 -----DL---LYWRDIK----- 184
 | | :| :|
 Db 752 PKKVKYKEVQLRRPNWSKFVAEDLSQDCFWTQVKEDRFENNELFAKLTILAFSAQTKTSKA 811

Qy 185 -----KT----- 186
 | |
 Db 812 KKDQEGGEEKSVQKKVKELKVLDSTAKQNLISIFLGSFRMPYQEIKNVILEVNEAVLTE 871

Qy 187 -----GVVFG-----ASLFLLLSLT 201
 | | | | | | | | | | | |
 Db 872 SMIQNLIKQMPPEPEQLKMLSELKEEYDDLAESEQFVVMGTVPRLRPRLNAILFKL---- 927

Qy 202 VFS-----IVSVTA-----YIALALL-----SVTISF- 223
 | | | | | | | :| | | | | | | | |
 Db 928 QFSEQVENIKPEIVSVTAACEELRKSENFSSLLELTLLVGNMAGSRNAGAFGFNISFL 987

Qy 224 ---RIYKGVIAI-----QKSDEGHP-----FRAYLESEVAISEELVQK----- 259
 | | | :| :| | | | :| :| :| :| :| :|
 Db 988 CKLRDTKSADQKMTLLHFLAELCENDHPEVLKFPDELAHVEKASRVSAENLQKSLDQMKK 1047

Qy 260 -----YSNSALGHVN--CTIKEL----- 275
 | :| :| | | | | | |
 Db 1048 QIADVERDVQNFPAAATDEKDKFVEKMTSFVKDAQEQYNKLRMMHSNMETLYKELGDYFVF 1107

Qy 276 -----RRLFL----- 280
 | :| |
 Db 1108 DPKKLSVEEFFMDLHNFRNMFLQAVKENQKRRETECKMRRAKLAKEKAERLEKQOKRE 1167

Qy 281 -----VDDLVDLKFVAVLMWVFTYVGFALFNGLTLLILALISLFSVPVIYER 326
 :| | :| :| :| | | | :|
 Db 1168 QLIDMNAEGDETGVMDSLLEALQ-----SGAAFR-----RKR 1199

Qy 327 HQAQIDHYLG-----LANKNVK-DAMAKIQAKIPGLKRKAE 361
 | :| | | :| :| | | | | :| :| :|
 Db 1200 GPRQVNRKAGCAVTSLLASELTKDDAMAPGPVKVP---KKSE 1238

Search completed: September 29, 2004, 18:56:38
 Job time : 27.0326 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:43:17 ; Search time 26.5368 Seconds
(without alignments)
1308.568 Million cell updates/sec

Title: SEQ29_1-172_990-1178
Perfect score: 1850
Sequence: 1 MEDLDQSPILVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Query Match	Length	ID	
1	827.7	44.7	776	2	A46583	neuroendocrine-spe
2	684.2	37.0	208	2	I60904	neuroendocrine-spe
3	666	36.0	267	2	A60021	tropomyosin-relate
4	454.3	24.6	2484	2	T26216	hypothetical prote
5	447	24.2	2607	2	T26215	hypothetical prote
6	353.5	19.1	222	2	T26213	hypothetical prote
7	275.1	14.9	1173	2	T31421	C-terminal domain-
8	266	14.4	1206	2	S24407	formin isoform IV
9	266	14.4	1468	2	S11515	formin - mouse
10	264.1	14.3	1058	2	T13286	cappuccino gene pr
11	262.4	14.2	1611	2	T38236	hypothetical prote
12	260.9	14.1	760	2	F86387	probable Pto kinas
13	257.1	13.9	3511	2	A59295	unconventional myo

14	256.5	13.9	1255	2	T31065	diaphanous protein
15	255.5	13.8	3530	2	A59266	unconventional myo
16	253.8	13.7	1132	2	A35098	MHC class III hist
17	253.6	13.7	1201	2	G86441	unknown protein [i
18	250.4	13.5	880	2	D89756	protein T23E7.2b [
19	250	13.5	980	2	S54986	regulatory protein
20	247.7	13.4	1015	2	JC6552	DNA topoisomerase
21	247.5	13.4	731	2	B86369	hypothetical prote
22	247.3	13.4	980	2	G75523	probable cell divi
23	247.2	13.4	1047	2	A55617	masquerade precurs
24	247	13.4	2090	2	S26058	probable transform
25	244.8	13.2	1127	2	T32404	hypothetical prote
26	244.8	13.2	1375	2	S48375	hypothetical prote
27	243.6	13.2	1721	1	I38902	retinoblastoma bin
28	243.4	13.2	3938	2	T42761	Bassoon protein -
29	243.3	13.2	708	2	D96711	hypothetical prote
30	243.3	13.2	786	2	A35466	progesterone recep
31	243	13.1	907	2	E96636	hypothetical prote
32	242.9	13.1	1634	2	T26517	hypothetical prote
33	242.6	13.1	716	2	T26998	hypothetical prote
34	241.5	13.1	933	1	QRHUP	progesterone recep
35	239.2	12.9	449	2	S16748	proline-rich prote
36	239.1	12.9	930	2	A25923	progesterone recep
37	238.7	12.9	1706	2	I84499	zinc finger protei
38	238.3	12.9	3149	1	QQBE8	BPLF1 protein - hu
39	237	12.8	1137	2	A86335	T20H2.9 protein -
40	236.9	12.8	710	2	D96728	hypothetical prote
41	236.7	12.8	2649	2	T51023	hypothetical prote
42	235.6	12.7	765	2	T49592	neurofilament trip
43	235.2	12.7	1953	2	S63244	BN11 protein - yea
44	235.1	12.7	534	2	S21961	proline-rich prote
45	234.8	12.7	993	2	T17230	hypothetical prote

ALIGNMENTS

RESULT 1

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 421-776 <ROE2>
A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309
C;Genetics:
A;Gene: GDB:RTN1; NSP
A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

Query Match 44.7%; Score 827.7; DB 2; Length 776;
Best Local Similarity 27.1%; Pred. No. 3.3e-20;
Matches 196; Conservative 55; Mismatches 89; Indels 383; Gaps 17;

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Qy      6 QSPL----- 9
      |||:
Db      70 QSPVAMETASTGVAGVSSAMDHTFSTTSKDGEAGSCYTSLSIDICYPPQEDSTYFTGILQK 129

Qy     10 ----VSSSDSPPR---PQP----- 21
      |: |:| | |
Db     130 ENGHVTISESPEELGTPGSPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKKILADPLDQM 189

Qy     22 ---AFKYQFVREPEDEEEEEEEEEDEDEDLE----- 50
      |:| | : | | : : | : | | | |
Db     190 KAEAYKYIDITRPEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDKPAPVEGKI 249

Qy     51 -----ELE----- 53
      | : |
Db     250 IKDHLLEESTFAPYIDDLSEEQRRAPQITTPVKITLTEIEPSVETTTQEKTPKQDICK 309

Qy     54 -----VLERKPAAGLS-- 64
      : | | | |
Db     310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEAKGLSYE 369

Qy     65 ----AAPV-----PTAPAAGAPL----- 78
      || | | | : | |
Db     370 TAENPRPVGQLADRPEVKARSGPPTIP---SPLDHEASSAESGDSEIELVSEDPMMAEDA 426

Qy     79 -----MDFGNDFVPPAPRGPLPAAPPV-----APE 103
      : | | : | | | | | : : |
Db     427 LPSGYVSFGHVGGPP---PSPASPSIQYSILREEREAEELDSLEIIESCDASSASEESPK 482

Qy    104 RQ---PSWDPSPVS-----STVPAPSPLSAAAVSP 130
      | : | | | : | | | | |
Db     483 REQDSPPMKPSALDAIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGP----- 534

Qy    131 SKLPEDD-----EPPARPPPPPPASVSPQAEPVWTPPAP-APAAPP-----STSVVDLL 178
      : | | | | | | | | | : | | | | | : | | |
Db     535 -ELPPGDGALEPETPMLPRKPEEDSSSNQSPAATKGPGLGPGAPPPLLFLNKQKAIDL 593

Qy    179 YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDE 238
      | | | | : | | | | : | | | | | | | | | | | | | | | | | | | | |
Db     594 YWRDIKQTGIVFGSFLLLFLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDE 653

Qy    239 GHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFT 298
      | | | | : | | : | | : | | : | | | | | | | | | | | | | | | |
Db     654 GHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKLRLFLVQDLVDLSLKFAVLMWLLT 713

```

Qy 299 YVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKR 358
 |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 714 YVGALFNGLTLLLMAVVSMTFLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKR 773

Qy 359 KAE 361
 ||
 Db 774 HAE 776

RESULT 2

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 37.0%; Score 684.2; DB 2; Length 208;
 Best Local Similarity 62.4%; Pred. No. 9.2e-17;
 Matches 131; Conservative 35; Mismatches 36; Indels 8; Gaps 1;

Qy 152 SPQAEPVWTPPAPAPAAPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAY 211
 | : : || : : : |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 7 STKMDCVW-----SNWKSQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVVSVVAY 58

Qy 212 IALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVNCT 271
 :||| || ||||| ||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 59 LALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNST 118

Qy 272 IKELRRLFLVDDLVDLSLKFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQI 331
 :||| ||||| ||||| |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 119 LKELRRLFLVQDLVDLSLKFAVLMWLLTYVVGALFNGLTLLLMAVVSMTFLPVVYVKHQAQI 178

Qy 332 DHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 | |||| : : : ||||| || ||
 Db 179 DQYLGLVRTHINAVVAKIQAKIPGAKRHAE 208

RESULT 3

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
 C;Accession: A60021
 R;Wieczorek, D.F.; Hughes, S.R.
 Brain Res. Mol. Brain Res. 10, 33-41, 1991
 A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
 A;Reference number: A60021; MUID:91278684; PMID:1647480
 A;Accession: A60021
 A;Molecule type: mRNA
 A;Residues: 1-267 <WIE>
 A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550
 C;Comment: This neuronal-specific mRNA was identified by hybridization to an
 alpha-tropomyosin probe but does not show homology in amino acid sequence.

Query Match 36.0%; Score 666; DB 2; Length 267;
 Best Local Similarity 66.1%; Pred. No. 7.3e-16;
 Matches 123; Conservative 34; Mismatches 29; Indels 0; Gaps 0;

```

Qy      172 TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIO 231
      :  :|||||||:|:|:|:| | | | | | | | | | | | | | | | | |
Db      10 SQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVLQ 69

Qy      232 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFA 291
      |:|:|:|:|:|:|:|:| | | | | | | | | | | | | | | | |
Db      70 AVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQLVNSTLKELRRLFLVQDLVDLSLKFA 129

Qy      292 VLMWVFYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA 351
      ||||: |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      130 VLMWLLTYVVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQVDQYLGLVVRTHINTVVAKIQA 189

Qy      352 KIPGLK 357
      ||||:
Db      190 KIPGAR 195

```

RESULT 4

T26216

hypothetical protein W06A7.3c - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26216

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26216

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2484 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3c

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 24.6%; Score 454.3; DB 2; Length 2484;
 Best Local Similarity 15.7%; Pred. No. 3.6e-06;
 Matches 126; Conservative 79; Mismatches 142; Indels 457; Gaps 18;

Qy 1 MEDLDQSPLVSSSDSPPR-----PQPAFKYQFV-----REPEDEEEEEE 38
 :| |:: : : || | :| | |::||
 Db 1679 VESLERPLTIITQQKPPEKPTEDIGALSPLSPNTLAEYEEVPMMDMQSVPHSPQEKQEEI 1738
 Qy 39 E-----EEE 42
 | |:
 Db 1739 EALSEIIIEEPQAMKEVEKPVESAPEKDNESLEAPEIINEPIRRVLVETKIMGPGKSLNED 1798
 Qy 43 EDEDED----- 48
 |::|
 Db 1799 NDDDDDGSECLDSIGDLSSERTIQRFNTSIDDPSIRRDSFSSISSFGDRQKFRTAIENIRQ 1858
 Qy 49 -----LEELEVLER 57
 ||:: :|
 Db 1859 DLLPFQSSVSQYLRSSPNPSQQLLVNLSMDSPSDLSPNAPPVGFENTAQFLEKLQQEDR 1918
 Qy 58 KPAAG-----LSAAPV----- 68
 | | :| ||
 Db 1919 PSAEGSIDSSGFEEKVDHEGLDEFAAPPVHDPMQKSVFGLSGSDDMKPGSQDDGFVFIERN 1978
 Qy 69 -----PTAPAAGAPLM----- 79
 ||| :|:
 Db 1979 EANEATLKKNQKMSSHNDVIEKNYFNDNAPTAALLESPIAEEARKLVQDAVESASEYKK 2038
 Qy 80 -----DFGNDFVPPA----- 89
 || :| || |
 Db 2039 QAVDSGDEIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGDFVHETVPNAVDDFVREAEK 2098
 Qy 90 --PRGPLP-----AAPP-----VAP--ERQP---- 106
 | |::| || ||| : :|
 Db 2099 QLPESFPVEKIETPEPLVDIHDTVDKVHDEVNDFLRREPTPPFETDDVAPLSDDKPQFGN 2158
 Qy 107 -----SWDPSPVSSTVPAPSPLSAAAVSPSK 132
 :|| |::| | || :
 Db 2159 QTPEEDETTFDRKGPLTIPEEVEKAAAAQNNDLDDFDPLVTSNTGAAFGAAGAAAVES 2218
 Qy 133 LPEDD-----EPPARPPPPP-----PASV-----SPQAEP-----V 158
 | |:: | ||| || |::| | : |
 Db 2219 LTEEEMFGHQKFETVPRPPTPPKDISDEDVKPSTVNLGPSHHHSHPSSPHHSILKHHGDA 2278
 Qy 159 W-----TPPAPAPAAPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA 213
 | || |:::|||| |:::| :| :| | :::| |
 Db 2279 WIDFKTVPPC-----VLDVIYWRDAKSAIVLSLALLLVFLVLAQYPLLTVVVYSL 2328
 Qy 214 LALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIK 273
 | | ||::| | |::| ||| | : : :| | : : | |
 Db 2329 LLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLPQEKVHAQADVFEHATCIAN 2388
 Qy 274 ELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDH 333
 :|::| | : :|::| :| : |::| | : :||| :| :| ||
 Db 2389 KLKKLVFVESPLESIKFGVLVLSLTYIASWFSGFTLAILGLLGVFSVPKVEYNQEAIDP 2448
 Qy 334 YLGLANKNVKDAMAKIQAKIPGLK 357
 :| : :|: | |::| :
 Db 2449 HLATISGHLKNVQNIIDEKLPFLR 2472

RESULT 5

T26215

hypothetical protein W06A7.3a - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26215

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26215

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2607 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3a

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
2586/2

Query Match 24.2%; Score 447; DB 2; Length 2607;
Best Local Similarity 14.0%; Pred. No. 7.3e-06;
Matches 128; Conservative 79; Mismatches 150; Indels 560; Gaps 18;

```

Qy      1 MEDLDQSPVLVSSSDSPPR-----PQPAFKYQFV-----REPEDEEEEE 38
      :| |::  : :  ||           |   :|: |           |:::|
Db      1679 VESLERPLTIITQQKPPEKPTEDIGALSPLSPNTLAEYEEVPMMDMQSVPHSPQEKQEEI 1738

Qy      39 E-----EEE 42
      |                               |:
Db      1739 EALSEIIEEPQAMKEVEKPVESAPEKDNESLEAPEIINEPIRRVLVETKIMGPGKSLNED 1798

Qy      43 EDEDED-----48
      |::|
Db      1799 NDDDDDGSECLDSIGDLSSERTIQRFNTSIDDPsirRDSFSSISSFGDRQKFRTAIENIRQ 1858

Qy      49 -----LEELEVLER 57
      ||::: :|
Db      1859 DLLPFQSSVSQYLRSSPNPSQQLLVTNLSMDSPDLSPNAPPVGFENTAQFLEKLQQEDR 1918

Qy      58 KPAAG-----LSAAPV-----68
      | |           :| ||
Db      1919 PSAEGSIDSSGFVKVDHEGLDEFAAPPVHDPMQKSVFGSLGSDDMKPGSQDDGFVFIERN 1978

Qy      69 -----PTAPAAGAPLM-----79
      |||   :|:
Db      1979 EANEATLKKNQKMSSHNDVIEKNYFNDNAPTAALLESPIAEEARKLVQDAVESASEYKK 2038

Qy      80 -----DFGNDFVPPA-----89
      || :: || |
Db      2039 QAVDSGDEIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGDFVHETVPNAVDDFVREAEK 2098

Qy      90 --PRGPLP-----AAPP-----VAP--ERQP----106
      | |::|           ||   ||| : :|
Db      2099 QLPESVPVEKIETPEPLVDIHDTVDKVHDEVNFLRREPTPPFETDDVAPLSDDKPQFGN 2158

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Qy 107 -----SWDPSPVSSTVPAPSPLSAAAVSPSK 132
 Db 2159 QTPEEDETTFDRKGPLTIPEEVEKAAAAQNNDLDDFDPLVTSNTGAAFGAAVGAAAAVES 2218
 Qy 133 LPEDD-----EPPARPPPPP-----PASV-----SPQAE-----V 158
 Db 2219 LTEEEMFGHQKFETVPRPPTPPKDISDEDVKPSTVNLGPSHHHSHPSPPHHSILKHHGDA 2278
 Qy 159 W-----TPPAPAPAAP----- 170
 Db 2279 WIDFKTVPPCAQNAFSPGEIMFLLAFFVYLSCFASFFSKSLPLLDNLLSLVVYLSISLII 2338
 Qy 171 ----- 170
 Db 2339 HVKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNIVLRVGLNVALVVGVAVSAHEAY 2398
 Qy 171 -----STSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVT 220
 Db 2399 KLTKSSGVLRRKKEVLDVIYWRDAKSAIVLSLALLVLFVLAKYPLLTVVVYSLLLALGAA 2458
 Qy 221 ISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFL 280
 Db 2459 AGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLPEQKVHAQADVFEHATCIANKLKKLVF 2518
 Qy 281 VDDLVDLSLKFAVLMWVFTTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANK 340
 Db 2519 VESPLESIKFGVLVLSLTYIASWFSGFTLAILGLLGVSVPKVYESNQEAIDPHLATISG 2578
 Qy 341 NVKDAMAKIQAKIPGLK 357
 Db 2579 HLKNVQNIIDEKLPFLR 2595

RESULT 6

T26213

hypothetical protein W06A7.3b - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26213

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26213

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-222 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3b

A;Map position: 5

A;Introns: 27/1; 77/2; 201/2

Query Match 19.1%; Score 353.5; DB 2; Length 222;
 Best Local Similarity 32.2%; Pred. No. 2.2e-05;
 Matches 65; Conservative 48; Mismatches 84; Indels 5; Gaps 1;

Qy	3	DLDDQSPLV-----	10
Db	52	DRDPMPLFPVPSLLPRLRAWRTGKTVSPQSHASRPACSRHLLTLGTGDGGPAPPPAPSSGS	111
Qy	11	-----SSSDSPPRPQP-----AF-----KYQ-----	26
		:	
Db	112	SSPSPSPSSSSSPPPPPPPPPPALPAPRFDIYDPFHPTDEAYSPPPAPEQKYDPFEAT	171
Qy	27	-----FVREPEDEEEEEEEEEED-----	44
		: : :	
Db	172	GSNPSSSGGTGPSPEEEEEEEEEEEGLSQSIRRISETLAGIYDDNSLSQDFPGDDSPHR	231
Qy	45	-----	44
Db	232	EPPPPOTLGAPGTPOADSTRAEGAPRRRVFVVVGPEAEACLEGKVSVEVVTTAGGPALPL	291

Qy	45	-----EDEDLEELEVL-----RKPAAG---LSAAPVPTAPAAGAPLM	79
		: : : : : : :	
Db	292	PPLPPTDPEIEEGEIVQPEEEPRVAVSLFRAARPRQPPASVATLASVAAPAAPPASAPRA	351
Qy	80	DFGNDFV-----PPAP-----R	91
		: :	
Db	352	PEGDDFLSLHADSDGEGALQVDLGEPPAPPAADARWGGLDLRRKILTQRRERYRQRSASP	411
Qy	92	GPLPAAPPVAPERQPSWDPSPVSS-----	115
		:	
Db	412	GPPPARKKARRERQRSGDPAPPDSPTWEAKKHSRERKLGSHSTARRRSRSRARRRSRSR	471
Qy	116	-----	115
Db	472	SADRRRGSHRSRSREKRRRRRRRSASPPPAASSSSSSRRERHRGKRREGGKKKKKRSRSRA	531
Qy	116	-----TVPAPSPLS-----	124
		:	
Db	532	EKRSGDLEKLPAPVPPSGSDRDSRRRGAVPPSIQDLTDHDLFAIKRTITVGRPDKTEPRA	591
Qy	125	---AAAVSPS-----	131
Db	592	PSPAPAVSPKGEVLYDSEGLSADERGAKGDKDRRRSGAASSSSSSREKASRRKALDGDRG	651
Qy	132	-----KLPEDDEP-----	139
		: :	
Db	652	RDRDRSSKKPRTPKDSAPGSGALPKAPPRSGSSSSSSSSCSRKVKLQSKVAVLIREGVSS	711
Qy	140	-----	139
Db	712	TTPAKDSSSSGLGSIGVKFSRDRESRSPFLKPDERSPAEGVKVAPGSTKPKKTKAKAKAG	771
Qy	140	-----	139
Db	772	AKKAKGTKGKTKPSKTRKKVRSGGSSTASGGPGSLKKSKADSCSQAASAKGTEETSWSGE	831
Qy	140	-----PARPPP---PPPASVSPQAEV---WTP-----	161
		: : : :	
Db	832	ERTTKAPSTPPPKVAPPPPALTTPDSQTVDSCKTPDVSFLAEEASEDTGVRVGAEEEEEEE	891
Qy	162	-----PAPAPAA-----PPSTS	173
		: :	
Db	892	EEEEEEEEEQQPATTTATSTAAAAPSTAPSAGSTAGDSGAEDGPAARASQLPTLPPP---	948
Qy	174	VVDLLYWR-----DIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG	228
		: : :	
Db	949	---MPWNLPAVDCTTSGV-----LALT-----ALLF-----	972
Qy	229	VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGH-----	267
		: : : :	
Db	973	-----KMEE-----ANLASR-AKAQELIQD-TNQILRHRKPPSTLGVTAPVPTSFGLP	1019
Qy	268	-----VNC-----TIKELRRLFLVDDL	285
		: :	
Db	1020	PAPSSYLLPGSLPIGGCGSTPPTPTGLVPASDKREGSSSSEGRGDTDKYLKKLHTQERAV	1079
Qy	286	DSLKFAVLMWVFTYVGFALNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDA	345

```

      : : |           | : | : :       : |           ||
Db      1080 EEVK-----LSIKPYYQKKDITKEEY-----KDI 1103

Qy      346 MAKIQAKI----- 353
      : | ||
Db      1104 LRKAVHKICHSKSGEINPVKVSNLVRAYVQRYRYFRKHGRKPGDPPGPPRPPKEPGPPDK 1163

Qy      354 --PGL 356
      |||
Db      1164 GGPGL 1168

```

RESULT 8

S24407

formin isoform IV - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C;Accession: S24407

R;Jackson-Grusby, L.; Kuo, A.; Leder, P.

Genes Dev. 6, 29-37, 1992

A;Title: A variant limb deformity transcript expressed in the embryonic mouse limb defines a novel formin.

A;Reference number: S24407; MUID:92112033; PMID:1339380

A;Accession: S24407

A;Molecule type: mRNA

A;Residues: 1-1206 <JAC>

A;Cross-references: EMBL:X62379; NID:g51552; PIDN:CAA44244.1; PID:g51553

```

Query Match          14.4%;  Score 266;  DB 2;  Length 1206;
Best Local Similarity 17.3%;  Pred. No. 1.6;
Matches 102;  Conservative 40;  Mismatches 97;  Indels 350;  Gaps 24;

```

```

Qy      5 DQSPLVSSSDSPPR-----PQPAFKYQFVREPEDEEE-----EEEEEE 41
      |||| :| | | | | | | | | | | | :| :
Db      459 DQSPTEQDDRTPGRLQAVWPPPKTK-----DTEEKVGLKYTEAEYQAAILHLKREHK 510

Qy      42 EEDE-----DEDLEEL-EVLERK----- 58
      || | :| :| | :| :| :
Db      511 EEIETLQAQFELKTFHIRGEHALVTARLEEAIEENLKQOLEKRREGCEEMRDVCISTDDDC 570

Qy      59 -PAA----- 61
      | |
Db      571 SPKAFRNVCIQTDRETFLKPCDAESKATRSSQIVPKKLTISLTQLSPSKDSKDIHAPFQT 630

Qy      62 --GLSA-----APVPTAPAAGAPLMDFGNDVFPPAP-----RGPLPAAPPVAPERQ 105
      | | : || || | | | :|| | |||| ||| : |
Db      631 REGTSSSSSQQKISPPAP-PTPPPLPPPL-----IPPPPLPPGLGPLPPAPPIPP--- 679

Qy      106 PSWDPSPVSSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPA-----SVSPQAEP 157
      ||| | | | | : :| | | | | | | | | |
Db      680 ----VCPVSPPPPPPPP-----PPTPVPPSDGPPPPPPPPPLPNVLALPNSGGPPPPPP 729

Qy      158 VWTTPAP--APAAPPSTSV-----VDLLYWRDIKKTGVVFGASLF 195
      || | || || | : |||
Db      730 PPPPPPPGLAPPPPPGLSFGLSSSSSQYPRKPAIEPSCPMKPLYWTR----- 776

Qy      196 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHP-----FRAY 245

```

```

          ||  || : |
Db      777 -----IQINDKSQDAAPT LWDSLEEPHIRT 802
Qy      246 LESEVAISEELVQ-----KYSNSA---LGHVNCTIKELRR 277
          | |  |:: |
Db      803 SEFEYLF SKDTTQKKKPLSEAYEKKNKVKKI KLLDGKRSQTVGILISSLHLEMKDIQQ 862
Qy      278 -LFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG 336
          :| |||
Db      863 AIFTVDD-----SVVDLET LAALYE----- 882
Qy      337 LANKNVKDAMAKIQ-----AKIPGLKRKAE 361
          |: :| : ||:
Db      883 --NRAQEDELTKIRKY YETSKEEDLKLLDKPEQFLHELAQIPNFAERAQ 929

```

RESULT 9

S11515

formin - mouse

C;Species: Mus musculus (house mouse)

C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C;Accession: S11515

R;Woychik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.

Nature 346, 850-853, 1990

A;Title: 'Formins': proteins deduced from the alternative transcripts of the limb deformity gene.

A;Reference number: S11515; MUID:90363291; PMID:2392150

A;Accession: S11515

A;Molecule type: mRNA

A;Residues: 1-1468 <WOY>

A;Cross-references: EMBL:X53599; NID:g52877; PIDN:CAA37668.1; PID:g52878

```

Query Match          14.4%; Score 266; DB 2; Length 1468;
Best Local Similarity 17.3%; Pred. No. 2.6;
Matches 102; Conservative 40; Mismatches 97; Indels 350; Gaps 24;

```

```

Qy      5 DQSPLVSSSDSPPR-----PQPAFKYQFVREPEDEEE-----EEEEEE 41
          |||| :| | | | | | | | | | | |
Db      685 DQSPT EQDDRTPGRLQAVWPPPKTK-----DTEEKVGLKYTEAEYQAAIHLHKREHK 736
Qy      42 EEDE-----DEDLEEL-EVLERK----- 58
          || | :| :| | : ||:
Db      737 EEIETLQAQFELKTFHIRGEHALVTARLEEAIENLKQOLEKRREGCEEMRDVCISTDDDC 796
Qy      59 -PAA----- 61
          | |
Db      797 SPKAFRNVCIQTDRETFLKPCDAESKATRSSQIVPKKLTISLTQLSPSKDSKDIHAPFQT 856
Qy      62 --GLSA-----APVPTAPAAGAPLMDFGNDFVPPAP-----RGPLPAAPPVAPERQ 105
          | |: || || | || :|| | ||| ||: |
Db      857 REGTSSSSQQKISPPAP-PTPPPLPPPL-----IPPPPLPPGLGPLPPAPPPIPP--- 905
Qy      106 PSWDPSPVSSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPA-----SVSPQAE 157
          ||| | | | : :| | | | | | | | |
Db      906 ----VCPVSPPPPPPP-----PPTPVPPSDGPPPPPPPPPLPNVLALPNSGGPPPP 955
Qy      158 WTPPPAP--APAAPPSTSV-----VDLLYWRDIKKTGVVFGASLF 195

```

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      || | || | |
Db      956 PPPPPPPGLAPPPPPGLSFGLSSSSSQYPRKPAIEPSCPMKPLYWTR----- 1002
Qy      196 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHP-----FRAY 245
      || || : |
Db      1003 -----IQINDKSQDAAPTLLWDSLEEPHIRT 1028
Qy      246 LESEVAISEELVQ-----KYSNSA---LGHVNCTIKELRR 277
      | | |:: |
Db      1029 SEFEYLFSDKDTTQQKKKPLSEAYEKKNKVKKIIKLLDGKRSQTVGILISSLHLEMKDIQQ 1088
Qy      278 -LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG 336
      :| |||
Db      1089 AIFTVDD-----SVVDLETIAALYE----- 1108
Qy      337 LANKNVKDAMAKIQ-----AKIPGLKRKAE 361
      |: :| : ||:
Db      1109 --NRAQEDELTKIRKYYETSKEEDLKLLDKPEQFLHELAQIPNFAERAQ 1155

```

RESULT 10

T13286

cappuccino gene protein - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C;Accession: T13286

R;Emmons, S.; Phan, H.; Calley, J.; Chen, W.; James, B.; Manseau, L.

Genes Dev. 9, 2482-2494, 1995

A;Title: Cappuccino, a *Drosophila* maternal effect gene required for polarity of the egg and embryo, is related to the vertebrate limb deformity locus.

A;Reference number: Z17651; MUID:96033799; PMID:7590229

A;Accession: T13286

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1058 <EMM>

A;Cross-references: EMBL:U34258; NID:g1061333; PID:g1061334; PIDN:AAC46925.1

C;Genetics:

A;Gene: capu

A;Cross-references: FlyBase:FBgn0000256

```

Query Match          14.3%; Score 264.1; DB 2; Length 1058;
Best Local Similarity 16.1%; Pred. No. 1.3;
Matches 118; Conservative 47; Mismatches 117; Indels 449; Gaps 27;

```

```

Qy      9 LVSSSDSPPR-----PQPAFKYQF-----VREPEDEEEEEEEEEEE---- 42
      |:|| | |||
Db      398 LLSSVDEPPRRPSKRCVNLTELLNASEATVYEYNKTGAEGCVKSFTDAETQTESEDCEGT 457
Qy      43 -----EDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFV-PP 88
      : || | || | || | | || |
Db      458 CKCGQSSTKVSDNKSATEDGE-----KPHA---VAPPPPPPPPLPA-----FVAPP 501
Qy      89 APRGPLPAAPPVAPERQPSWDPSVSTVPAPSPLSAAAVSPSKLPEDDEPPAR----- 142
      | | | ||:| | | | | | | :| | |||
Db      502 PPPPPPPPPPLANYGAP---PPP-----PPPPPGSGSAPPP-----PPPAPIEGGGG 546
Qy      143 -PPPPPPASVSPQAEFV-----WT----- 160

```



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      ||||| | | :
Db      547 IPPPPPPMSASPSKTTISPAPLPDPAEGNWFHRTNTMRKSAVNPPKPMRPLYWTRIVTSA 606
Qy      161 PPAP-----APAAPPSTSVVDLLYWRDIKKT---- 186
      |||| | |||:| : | :||:|
Db      607 PPAPRPPSVANSTDSTENSGSSPDEPPAANGADAPPTAPPATKEI----WTEIEETPLDN 662
Qy      187 -----GVVF----- 190
      |:::
Db      663 IDEFTELFSRQAIAPVSKPKELKVKRAKSIKVLDPERSRNVGIIWRS LHPVSPSEIEHAIY 722
Qy      191 -----GASLFL-----LLSLTVFSI----VSV 208
      | : | || ::| : :|
Db      723 HIDTSVVSLEALQHMSNIQATEDELQRIKEAAGGDIPLDHPEQFLLDISLISMASERISC 782
Qy      209 TAYIALALLSVTISFRIYKGVIAIQ----- 234
      : | |||: || : | | |
Db      783 IVFQAEFEESVTLLFRKLETVSQLSQQLIESED LKLVFSIILTLGNYMNGGNRQRGQADG 842
Qy      235 -----KSDEGH----- 240
      || | |
Db      843 FNLDILGKLKDVKSKESH TLLHFIVRTYIAQRRKEGVHPLEIRLPIPEPADVERAAQMD 902
Qy      241 -----PFRAYLESEVAISEELVQKYSNSAL 265
      ||::: :| | ::::| | |
Db      903 FEEVQQQIFDLNKKFLGCKRRTAKVLAASRPEIMEPFKSKMEEFVEGADKSMAKLHQS-- 960
Qy      266 GHVNCTIKELRRLFL-----VDDLVD SLKFAVL 293
      : | | ||| :| | |
Db      961 -----LDECRDLFLETMRFYHFSPKACTLT LAQCTPDQFFEYWTNFTNDFKDIWK---- 1010
Qy      294 MWVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK---IQ 350
      : :| | | : : ||||: : :|| : | |
Db      1011 ----KEITSLNLNEL-----MKKSKQAQIE-----SRNRNVSTKVEKSGRIS 1046
Qy      351 AKIPGLKRKAE 361
      | | |:::
Db      1047 LKERMLMRRSK 1057

```

RESULT 11

T38236

hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T38236

R;Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, February 1998

A;Reference number: Z21780

A;Accession: T38236

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1611 <MUR>

A;Cross-references: EMBL:AL021813; PIDN:CAA16991.1; GSPDB:GN00066;

SPDB:SPAC23A1.17

A;Experimental source: strain 972h-; cosmid c23A1

C;Genetics:

A;Gene: SPDB:SPAC23A1.17

A;Map position: 1

Query Match 14.2%; Score 262.4; DB 2; Length 1611;
Best Local Similarity 9.8%; Pred. No. 4.4;
Matches 127; Conservative 57; Mismatches 112; Indels 1006; Gaps 29;

```
Qy      2 EDL-----DQSPLV-----SSSDSPPRP----- 19
      |:|      | | |      :|| | :|
Db      299 EELSKSQRVAKDDDDPFVVSNTANSDEPASSSSKPAKPLTDLNRAFSQRLNLDLPQKPGKSQG 358

Qy      20 -----QPAFKYQFVREPEDEEE-----EEEEEEEEDEDEDL 49
      | : : | ||| : : | | | : | | : |
Db      359 EISEQEEDEYDDAESDEMHSPPYSTHEPESEPEDQDEPSEKDDENKDVVEEQEQEQEQEQEQEI 418

Qy      50 EELE-----VLERKPAAG----- 62
      : | | | |
Db      419 DPEEAKRIALRERMAKMSGGIGMHVFGLPGLAAPIGRKNTLRRTPAKSSEEAKSTTNDSS 478

Qy      63 ----- 62
Db      479 PPKDSSSTSTQPTESNAQQAPSPKEEERPLPSEPSQNQPAEYRDTPTDTPRNIMPLPGLM 538

Qy      63 -----LSA 65
      ||
Db      539 SADQPIKVTEPSNDADKAIVAEGPNNEEETKGPVIPETQETSEQQVHKTPSPEKQKVLSP 598

Qy      66 APV-----PTAP----- 72
      | : | : |
Db      599 PPIITNFDKETLASNEAHEAVPQKPSAPQVTRLMAPQDSSSVVTPSPTSLLDPAVARVKV 658

Qy      73 -----AAGAPL----- 78
      || : :
Db      659 IDGIDPPKEAGAGATADVESAANSPIPTPRTWHSPDFTSKSFEPKLPKPSRISEVTEDS 718

Qy      79 -----MDFGN-----DFVPPAPR----- 91
      : || | : | ||
Db      719 IDEDKQNEVDPSTSARALPPPGLRFGKVDTLASLAHDDLDDLPVPRIFSPPLPKTPSG 778

Qy      92 -----GP 93
      |
Db      779 EFGDNEFMFPKKSNNRVRGHQSRPSTGSQRLNVVPVSIIVTSGGRPAPLPDEMASPSSSIGHP 838

Qy      94 LPAAPPV-----APERQPSWD-----PSPVSST----- 116
      || : || | | | : : | : | : : |
Db      839 LPSPPPADFNLSLVDFYEPHSYLESPAPEPQPSYEEESFNATVIHAPTPTSTATFQGHPTI 898

Qy      117 ----- 116
Db      899 SNVATPPLKQDVTESKASPVADASATHQSSTGLTQEITQLGSNMRLPTKLTRPSNDGRKA 958

Qy      117 -----VPAPSPLSAAAVSPSKLPEDDEPPARP----- 143
      : | | | : | | : | | | : |
Db      959 SGPRPAAPPSIPPPLVPSNILSSPTSEPPKDHPSPAPLSKPVSTSPAAPLARVPPVPKLS 1018

Qy      144 -----PPPPASVSPQAE--- 156
      ||| || | : |
```

Db 1019 SKAPPVPLPSADAPPPIVPSTAPPVPIPTSTPPVPKSSSGAPSAPPPVPA---PSSEIPS 1075
 Qy 157 ---PVWTPPPAPAP----- 166
 | | | |
 Db 1076 IPAPSGAPPVPAPSGIIPPVPKPSVAAPPVPKPSVAVPPVPAPSGAPPVPKPSVAAPPVPV 1135
 Qy 167 -----AAPP----- 170
 | | | |
 Db 1136 PSGAPPVPKPSVAAPPVPAPSGAPPVPKPSVAAPPVPAPSSGIPPVPKPAAGVPPVPPPS 1195
 Qy 171 ----- 170
 Db 1196 EAPPVPKPSVGVPPVPPPSTAPPVPTPSAGLPPVPVPTAKAPPVPAPSSEAPSVSTPRSS 1255
 Qy 171 ----- 170
 Db 1256 VPSPHSNASPSPTSSSMASAPARTSVSRSKSKAERHETSTSSRKSSKSGEHHHHHNEGH 1315
 Qy 171 --STSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF-----SIVSVTAYI----- 212
 | : | | : | : | | | : | | | |
 Db 1316 ADSSSTRTSLAHQDSRK-----SLHRHLSRSSSRASKKPSIVSTTGPFNFSFAKPVE 1368
 Qy 213 -----ALALLSVTISFRIYKGV----- 229
 : : : : | : :
 Db 1369 PCASEKWWLNSTAVPKSVVQMNDVLYMIKEGITGQDKKYKSVHILFPDYSQTVLTATFN 1428
 Qy 230 -----IQAIQKSDEGHPFRAYLESEVAISEELVQK----YSNSALGHVNCTIKELRR 277
 : : | : | : | : | : | :
 Db 1429 PHNQNTQLSQLQLAPPAQPSKARLDEEYACYGSTILKKARAYQGSVMVGDS----- 1480
 Qy 278 LFLVDDLVDLKFVAVLMWVFTYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYL-- 335
 | : | : : | | | | |
 Db 1481 -----AFTFVNSVMS-----ILA-----HNLEP 1498
 Qy 336 -----GLANKNV-----KDAMAKIQAKIPGLK 357
 | : | | | : : | | |
 Db 1499 INKQTFGGVIYKVNVTQVQIGIIRPGDIVTFDKAKFSGQK 1540

RESULT 12

F86387

probable Pto kinase interactor [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: F86387

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.;
 Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.;
 Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.;
 Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.;
 Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.;
 Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.;
 Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-
 Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu,
 S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Miranda,

M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: F86387

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-760 <STO>

A;Cross-references: GB:AE005172; NID:g11079512; PIDN:AAG29223.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1

Query Match 14.1%; Score 260.9; DB 2; Length 760;
Best Local Similarity 15.2%; Pred. No. 0.72;
Matches 119; Conservative 57; Mismatches 127; Indels 481; Gaps 27;

Qy 2 EDLDQSPVLVSSSDSP-----PRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVL 56
|:: || | || | ||:| |

Db 10 EEVSLSP---SLASPPLMALPPPQSPFPGDNATSP-----T 42

Qy 57 RKPAAG-----LSAAPVPTAPAAAGAPLMDFGNDFVPPAP--RGPLPAAPPVAPERQ 105
|:| | :| | : | : ||:| || | ||:| :

Db 43 REPTNGNPPETTTNTPAQSSPPPETPLSSPP-----PEPSPPSPSLTGPPPTTIPVSPPE 97

Qy 106 PSWDP-----SPVSS-----TV 117
|| | :||| :

Db 98 PSPPPPLPTEAPPPANPVSSPPPESSPPPPPPTEAPPTTPTITSPSPPTNPPPPESPPSL 157

Qy 118 PAPSPLS-----AAAVSPSKLPEDDEPP 140
||| | | : || | | | |

Db 158 PAPDPPSNPLPPPKLVPSSHSPRHLPSPPASEIPPPRHLPSPPASERPSTPPSDSEHP 217

Qy 141 ARPP-----PPPPASVSPQAE-----VWTPPAPAP----- 166
: || ||| | | | || |:

Db 218 SPPPPGHPKRREQPPPPGSKRPTSPSPSPDSKRPVHPSPPSPPEETLPPPKPSPDPLPS 277

Qy 167 -----AAPPS-----TSVVDLLYWRDIKKTGVVFGASLF 195
: || | | | : :|:

Db 278 NSSSPPTLLPPSSVVSPPSPPRKSVSGPDNPSNNPTPVT-----NSSSSGI----- 325

Qy 196 LLSLTVFSIVSVTAYIALALLSV----- 219
:: :| | : || ||::

Db 326 -----SIAAVGVSIGVALVLLTLIGVVVCLKKRKKRLSTIGGGYVMPTPMESSSPRSD 380

Qy 220 -----TISF----- 223
| |

Db 381 SALLKTQSSAPLVGNRSSNRTYLSQSEPGGFGQSRELFSEELVIATNGFSDENLLGEGG 440

Qy 224 --RIYKGV-----IQAIQKSDEG-----HPFRAYLESEVAISEELVQKYSNSALGHVNCT 271
|:|||| : |:: | |:| :: : : : | |

Db 441 FGRVYKGVLPDERVVAVKQLKIGGGQGDREFKAEVDT-----ISRVRHNRNLLSMVGYC 493

Qy 272 IKELRRLFLVD-----DLVDSLKFV----- 292

```

      | | | | : |           | : | |
Db      494 ISENRRLLIYDYVPNNNLYFHLHGTPGLDWATRVKIAAGAARGLAYLHEDCHPRIIHRDI 553
Qy      293 -----LMWVFETYVG---ALFNGLT----- 308
      : | | | : | |
Db      554 KSSNILLENNFHALVSDFGLAKLALDCNTHITTRVMGTFGYMAPEYASSGKLTEKSDVFS 613
Qy      309 --LLILALIS-----LFSVPVIYERHQAQIDHYLG----- 336
      :: | | : | | | | |
Db      614 FGVVLEELITGRKPVDSQPLGDESLVEWARPLLSNATETEEFTALADPKLGRNYVGVEM 673
Qy      337 -----LANKNVKDAM-----AKIQAKIPGL 356
      | | :: : | | : |
Db      674 FRMIEAAAACIRHSATKRPRMSQIVRAFDSLAEEDLTNGMRLGESEIINSAQQSAEIRLF 733
Qy      357 KRKA 360
      : | |
Db      734 RRMA 737

```

RESULT 13

A59295

unconventional myosin-15 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000

C;Accession: A59295

R;Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Miller, W.; Touchman, J.W.; Jin, L.; Sullivan, S.L.; Sellers, J.R.; Camper, S.A.; Lloyd, R.V.; Kachar, B.; Friedman, T.B.; Fridell, R.A.

Genomics 61, 243-258, 1999

A;Title: Characterization of the human and mouse unconventional myosin XV genes responsible for hereditary deafness DFNB3 and shaker 2.

A;Reference number: A59266; MUID:20021762; PMID:10552926

A;Accession: A59295

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-3511 <LIA>

A;Cross-references: GB:AF144095; NID:g6224684; PIDN:AAF05904.1; PID:g6224685

C;Genetics:

A;Gene: MGI:Myo15

A;Cross-references: MGI:1261811

A;Map position: 11:33.9

C;Superfamily: myosin motor domain homology

F;1209-1871/Domain: myosin motor domain homology <MMO>

Query Match 13.9%; Score 257.1; DB 2; Length 3511;

Best Local Similarity 9.5%; Pred. No. 48;

Matches 136; Conservative 46; Mismatches 113; Indels 1139; Gaps 35;

```

Qy      16 PPRP-----QPAFKYQFV-----REPEDEEEEE----- 37
      | | : | | | : | | | |
Db      388 PGMPYVYPEEPAFMYPWPVPPPIIMSPHNPYAHPMDDIAELEEPEETGEERQSTSFRLLPSAA 447
Qy      38 -----EEEEEE 43
      | | | |
Db      448 FFEQQGMDKPARSKLSLIRKFRLFPRPQVKLFGKEKLEVPLPPSLDIPLPLGDAGEEEEE 507

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Qy	44	DEDEDLEEEVLERKPAAGLSAAPVPTAP-----AAGAPL-MDF	81
		:	
Db	508	EE-----MPPVPTMPYTHPYWSFLTTPRQRNLQRALSAFGARQGLGF	548
Qy	82	GNDFVPPAPR-----GPLP-----AAPPVA-----	101
		:	
Db	549	GPEFGHPTPRPATSLARFLKKTLSSEKKPIPRLRGSQKARGGRPPVREAAAYKRFGYKLAGM	608
Qy	102	-PER-----QPSWDPSP-----VSSTVPAPSPLSAAAVS	129
		:	
Db	609	DPDRNTPIVLRRSQPQARNNNNSHGPPSPRPAPRALTHWSALISPPMPAPSPSPASPLT	668
Qy	130	-----	129
Db	669	PPFSPTFSRPPRLASPYGSLRQHPPPWAAPAHVFPFPQANWWGFAEPPGTSPEVAPDLLA	728
Qy	130	-----	129
Db	729	FPVPRPSFRASRSRRAAYGFPSPSLIGSRRRPHLPSPQPSLRSLPGQGYHSPLGPLSP	788
Qy	130	-----	129
Db	789	QLSLRRGPFQPPFPPPPRRPQSLREAFSLRRASGRLGPPRSPVLGSPRPPSPPPLLKHGP	848
Qy	130	-----PSKLPED-----DEPPAR-----PPPP-----	146
		:	
Db	849	RHRSLNLPSRLPRTWRRLSEPPTRAVKPWVHRAYPPPPSAGPWGASTGALEQQENQREAE	908
Qy	147	-----PPA-----SVSP	153
		:	
Db	909	DSETPWTVPPLAPSWDMDPPTQRPPSPWPEGIGSLRGFSRPPVPENPLLEHTSPSCEP	968
Qy	154	QAE-----	156
		:	
Db	969	QSEDRVSNLTGIFLGQHHDPGPGQLTKSADPSLEKPEEVVTLGDPQPPAEPEALNPTPPN	1028
Qy	157	-----PVW-----	159
Db	1029	KNVVSERKVLRLSASYPLVTCKQARATWPQWHRWKTVSRTAPLAPTRAPGPLLKAGEQP	1088
Qy	160	-----TPPAPAPAAP-----	170
Db	1089	RAEPGRFAVVMPPQVRGVSSFRPKGPAVPQPEHPDQDPEQGPAQACSLRWPCLPPTDA	1148
Qy	171	-----STSV	174
Db	1149	HCLWSRIRTYSSQSHLRGHGGDCHKSLWKKTRPQSWQNMHSIRNLPSMRSREQHREDGV	1208
Qy	175	VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ	234
		: : :	
Db	1209	EDMTQLEDLQETTVL--ANL-----KTRFERNLITYIGSILVSV-----	1246
Qy	235	KSDEGHPFRAYLESEVAISEELVQKYSNSALG-----	266
		: :	
Db	1247	-----NPYRMF-----AIYGPEQVQYSGRALGENPPHLFAIANLAFKMLDAKQNCVII	1297
Qy	267	-----	266

```

Db      1298 SGESGSGKTEATKLILRCLAAMNQRRDVMQQIKILEATPLLEAFGNAKTVRNDNSSRFGK 1357
Qy      267 -----HV----- 268
                |:
Db      1358 FVEIFLEGGVICGAITSQYLLEKSRIVFQAKNERNYHIFYELLAGLPAQLRQAFSLQEAE 1417
Qy      269 -----NCTI-----KELRRLF----- 279
                || | : |||
Db      1418 TYYYLNQGGNCEIAGKSDADDFRLLAAMEVLGFTSEDQDSIFRILASILHLGNVYFEKH 1477
Qy      280 -----LVD--D 283
                || |
Db      1478 ETDAQEVASVVSAREIQAVAELLQVSPEGLQKAITFKVTETIREKIFTPLTVESAVDARD 1537
Qy      284 LVDSLKFVILM-WVFTYVGAL-----FNGLTLLIL-----ALI 315
                : : :| | : | | || || | : |
Db      1538 AIAKVLVYALLFGWLITRVNALVSPKQDTLSIAILDYGFEDLSFNSFEQLCINYANENLQ 1597
Qy      316 SLFSVPVIYERHQAQ----- 330
                ||: :::: | :
Db      1598 YLFN-KIVFQEEQEEYIREQMDWREIAFADNQPCINLISLKPYGILRILDDQCCFPQATD 1656
Qy      331 -----IDHYLGLANKNV-----KDAM----- 346
                | | | | : | :
Db      1657 HTFLQKCHYHHGANPLYSKPKMPLPEFTIKHYAGKVTYQVHKFLDKNHDQVRQDVLDLFLV 1716
Qy      347 -----AKIQAKIPGLKRKAE 361
                || | : | | |
Db      1717 HSRTRVVAHLFSSHAAQTAPPRLGKSSSITRLYKAHTVAAKFQQSLLDLVEKME 1770

```

RESULT 14

T31065

diaphanous protein homolog p140mDia - mouse

C;Species: Mus musculus (house mouse)

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C;Accession: T31065

R;Watanabe, N.; Madaule, P.; Reid, T.; Ishizaki, T.; Watanabe, G.; Kakizuka, A.; Saito, Y.; Nakao, K.; Jockusch, B.M.; Narumiya, S.

EMBO J. 16, 3044-3056, 1997

A;Title: P140mDia, a mammalian homolog of Drosophila diaphanous, is a target protein for Rho small GTPase and is a ligand for profilin.

A;Reference number: Z20961; MUID:97357293; PMID:9214622

A;Accession: T31065

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1255 <WAT>

A;Cross-references: EMBL:U96963; NID:g2114472; PID:g2114473; PIDN:AAC53280.1

A;Note: binds to GTP-bound form of Rho and binds to profilin

Query Match 13.9%; Score 256.5; DB 2; Length 1255;

Best Local Similarity 14.7%; Pred. No. 3.7;

Matches 130; Conservative 42; Mismatches 135; Indels 575; Gaps 31;

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Qy      6 QSPLVSSSDSPRPQ-----PAF----- 23
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Db 406 QHLLLVRNDYEARPQYYKLIEECVSQIVLHKNGTDPDFKCRHLQIDIERLVDQMIDKTKV 465
 Qy 24 -----KYQFVREP 31
 Db 466 EKSEAKATELEKKLDSELTARHELQVEMKKMENDFEQKLQDLQGEKDALDSEKQQITAQK 525
 Qy 32 EDEEEEE-----EEEEDEDEDLEEEVLERKPAAGLSAAPVPTAPAAAGAPLMDF 81
 Db 526 QDLEAEVSKLTGEVAKLSKELEDAKNEMASLSAVVAPSVSSSAAVPPAPPLPG---DS 581
 Qy 82 GNDFVPPAPRGPLPA-----APPVAP----- 102
 Db 582 GTVIPPPPPPPPLPGGVPPSPPLPPGTCIPPPPPPLPGGACIPPPPPQLPGSAAIPPPPPPL 641
 Qy 103 ---ERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARP----- 143
 Db 642 PGVASIPPPPPPLPGATAIPPPPPPLPGATAIP-----PPPPPLPGGTGIPPPPPPLPGSV 694
 Qy 144 ---PPPPPPASVSPQAEVWTPPAPAPAAP-----PSTSVV----- 175
 Db 695 GVPPPPPLPGGPGGLPP---PPPPFFGAPGIPPPPPGPGVPPPPPPFGFGVPAAPVLPFGLT 751
 Qy 176 -----DL---LYWRDIK----- 184
 Db 752 PKKVKPEVQLRRPNWSKFVAEDLSQDCFWTQVKEDRFENNELFAKLTLAFSAQTKTSKA 811
 Qy 185 -----KT----- 186
 Db 812 KKDQEGGEEKSVQKKVKELKVLDSKTAQNLSIFLGSRMPYQEIKNVILEVNEAVLTE 871
 Qy 187 -----GVVFG-----ASLFLLLSLT 201
 Db 872 SMIQNLIKQMPPEPEQLKMLSELKEEYDDLAESEQFGVVMGTVPRLRPRLNAILFKL---- 927
 Qy 202 VFS-----IVSVTA-----YIALALL-----SVTISF- 223
 Db 928 QFSEQVENIKPEIVSVTAACEELRKSENFSLSLELTLLVGNMAGSRNAGAFGFNISFL 987
 Qy 224 ---RIYKGVIQAI-----QKSDEGHP-----FRAYLESEVAISEELVQK----- 259
 Db 988 CKLRDTKSADQKMTLLHFLAELCENDHPEVLKFPDELAHVEKASRVSAENLQKSLDQMKK 1047
 Qy 260 -----YSNSALGHVN---CTIKEL----- 275
 Db 1048 QIADVERDVQNFPAAATDEKDKFVEKMTSFVKDAQEQYNKLRRMMHSNMETLYKELGDYFVF 1107
 Qy 276 -----RRLFL----- 280
 Db 1108 DPKKLSVEEFFMDLHNFRNMFQAVKENQKRRETEEKMRRAKLAKEKAKEKERLEKQOKRE 1167
 Qy 281 -----VDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYER 326
 Db 1168 QLIDMNAEGDETGVMSLLEALQ-----SGAAFR-----RKR 1199
 Qy 327 HQAQIDHYLG-----LANKNVK-DAMAKIQAKIPGLKRKAE 361
 Db 1200 GPRQVNRKAGCAVTSLLASELTKDDAMAPGPVKVP---KKSE 1238

RESULT 15

A59266

unconventional myosin-15 - human

C;Species: Homo sapiens (man)

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 08-Sep-2000

C;Accession: A59266

R;Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Miller, W.; Touchman, J.W.; Jin, L.; Sullivan, S.L.; Sellers, J.R.; Camper, S.A.; Lloyd, R.V.; Kachar, B.; Friedman, T.B.; Fridell, R.A.

Genomics 61, 243-258, 1999

A;Title: Characterization of the human and mouse unconventional myosin XV genes responsible for hereditary deafness DFNB3 and shaker 2.

A;Reference number: A59266; MUID:20021762; PMID:10552926

A;Accession: A59266

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-3530 <LIA>

A;Cross-references: GB:AF144094; NID:g6224682; PIDN:AAF05903.1; PID:g6224683

C;Superfamily: myosin motor domain homology

F;1225-1887/Domain: myosin motor domain homology <MMO>

Query Match 13.8%; Score 255.5; DB 2; Length 3530;
Best Local Similarity 9.9%; Pred. No. 55;
Matches 140; Conservative 41; Mismatches 125; Indels 1105; Gaps 36;

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Qy      42 -----EEDEDEDLEEL----- 52
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Db      476 KFRLFPRPQVKLFGKEKLEVPLPPSLDIPLPLGDADEEEDDEELPPVSAVPYGHFPWGFL 535

Qy      53 -----EVLERKPAAGLS----- 64
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Db      536 TPRQRNLQRALSAFGAHRGLGFGPEFGRPVPRPATSLARFLKKTLSSEKKPIARLRGSQKT 595

Qy      65 ----- 64

Db      596 RAGGPAVREAAYKRFGYKLAGMDPEKPGTPIVLRRAQPRARSSNDARRPPAPQPAPRTLS 655

Qy      65 -----AAP--VPTAPA 73
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Db      656 HWSALLSPPVPPRPPSSGPPAPPLSPALSGLPRPASPYGSLRRHPPPWAAPAHVPPAPQ 715

Qy      74 AG-----APLMD 80
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Db      716 ASGWAFVEPPAVSPEVPPDLLAFPGPRPSFRGSRRRGAAGFGPGASPRASRRRAWSPLAS 775

Qy      81 -----FGNDFVPPA----- 89
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Db      776 PQPSLRSSPGLGYCSPLAPPSPQLSLRTGPFQPPFLPPARRPRSLQESPAPRRAAGRLGP 835

Qy      90 -----PRGPLPAAPPV----- 100
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Db 836 PGSPLPGSPRPPSPPLGLCHSPRRSSLNLP SRLPHTWRRLSEPPTRAVK PQVRLPFH RPP 895
 Qy 101 -----APERQPSWD----- 109
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 Db 896 RAGAWRAPLEHRESPREPEDSETPWTVPPLAPSWDVDM PPTQRPPSPWPGGAGSRRGFSR 955
 Qy 110 PSPVSSTV-----PAPSP-----LSAAAVSPSK----- 132
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 Db 956 PPPVPENPFLQLLGPVPSPTLQPEDPAADMTRVFLGRHHEPGPGQLTKSAGPTPEKPEEE 1015
 Qy 133 -----LPEDDEPPARPPP----- 145
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 Db 1016 ATLGDPQLPAETKPPTPAPPKDVTPPKDITPPKDVLP EQKTLRPSLSYPLAACDQTRATW 1075
 Qy 146 PP-----PASV 151
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 Db 1076 PPWHRWGTLPQAAAPLAPIRAPEPLPKGGERRQAAPGRFAVVM PRVQKLSSFQRVGPATL 1135
 Qy 152 SPQAEPVWTP-----PAP-----APAA----- 168
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 Db 1136 KPQVQPIQDPKPRACSLRW SCLWL RADAYGPWPRVHTHPQSCHLGPGAACLSLRGSWEEV 1195
 Qy 169 -PPS-----TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSI 205
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 Qy 206 VSVT-----AYIALALLSVT--ISFRIYKGVIAIQKSDEGHFPFRAYLESEVAISEEL 256
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 Db 1242 LKIRFERNLIIYTYIGSILVSVNPYQMFGIY-----GPEQ 1275
 Qy 257 VQKYSNSALG----- 266
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 Db 1276 VQQYNGRALGENPPHLFAVANLAFAKMLDAKQNCIIISGESGSGKTEATKLILRYLAAM 1335
 Qy 267 ----- 266
 Db 1336 NQKREVMQQIKILEATPLLESFGNAKTVRNDNSSRF GK FVEIFLEGGVISGAITSQYLLE 1395
 Qy 267 -----HV-----NCTI-----KEL 275
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 Db 1396 KSRIVEQAKNERNYHIFYELLAGLPAQLRQAFSLQEAETYYYYLNQGGNCEIAGKSDADDF 1455
 Qy 276 RRLF----- 279
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 Db 1456 RRLLAAMEVLGFSSSEDQDSIFRILASILHLGNVYFEKYETDAQEVASVVSAREIQAVAE L 1515
 Qy 280 -----LVD--DLVDSLKFAVLM-WVFTYVGAL- 303
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 Db 1516 LQISPEGLQKAITFKVTETMREKIFTPLTVESA VDARDAIAKVLYALLFSWLITRVNALV 1575
 Qy 304 -----FNGLTLLIL-----ALISLFSVPVIYERHQ-----AQID- 332
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 Db 1576 SPRQDTLSIAILDYGFEDLSFNSFEQLCINYANENLQYLFNKIVFQEEQEYIREQIDW 1635
 Qy 333 ----- 332
 Db 1636 QEITFADNQPRINLISLKPYGILRILDDQCCFPQATDHTFLQKCHYHHGANPLYSKPKMP 1695

Qy 333 -----HYLGLANKNV-----KDAM----- 346
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 Db 1696 LPEFTIKHYAGKVTYQVHKFLDKNHDQVRQDVLDLFVRSRTRVVAHLFSSHAPQAAPQRL 1755
 Qy 347 -----AKIQAKIPGLKRKAE 361
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Search completed: September 29, 2004, 18:55:49
 Job time : 33.5368 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:54:54 ; Search time 86.1193 Seconds
(without alignments)
1348.937 Million cell updates/sec

Title: SEQ29_1-172_990-1178
Perfect score: 1850
Sequence: 1 MEDLDQSPVLVSSSDSPPRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	1833.8	99.1	373	9	US-09-789-386-6	Sequence 6, Appli
2	1833.8	99.1	373	9	US-09-765-205-6	Sequence 6, Appli
3	1833.8	99.1	373	9	US-09-893-348-24	Sequence 24, Appl
4	1833.8	99.1	373	12	US-10-408-967-8	Sequence 8, Appli
5	1833.8	99.1	373	14	US-10-060-036-72	Sequence 72, Appl
6	1825.8	98.7	373	16	US-10-466-258-4	Sequence 4, Appli
7	1756.9	95.0	1192	9	US-09-789-386-2	Sequence 2, Appli
8	1756.9	95.0	1192	9	US-09-758-140-6	Sequence 6, Appli
9	1756.9	95.0	1192	9	US-09-893-348-23	Sequence 23, Appl
10	1756.9	95.0	1192	9	US-09-972-599A-6	Sequence 6, Appli
11	1756.9	95.0	1192	12	US-10-267-502-429	Sequence 429, App
12	1756.9	95.0	1192	14	US-10-060-036-71	Sequence 71, Appl
13	1756.9	95.0	1192	16	US-10-327-213-9	Sequence 9, Appli
14	1756.9	95.0	1192	16	US-10-466-258-9	Sequence 9, Appli
15	1749.9	94.6	1192	12	US-10-408-967-7	Sequence 7, Appli
16	1556.2	84.1	379	14	US-10-205-194-164	Sequence 164, App
17	1546.3	83.6	360	9	US-09-893-348-20	Sequence 20, Appl
18	1478.8	79.9	1163	9	US-09-893-348-18	Sequence 18, Appl
19	1441.2	77.9	1163	12	US-10-267-502-431	Sequence 431, App
20	927	50.1	199	9	US-09-893-348-25	Sequence 25, Appl
21	927	50.1	199	12	US-10-660-946-1	Sequence 1, Appli
22	920	49.7	199	12	US-10-408-967-9	Sequence 9, Appli
23	918	49.6	199	12	US-09-978-360A-467	Sequence 467, App
24	904	48.9	199	9	US-09-893-348-21	Sequence 21, Appl
25	886	47.9	199	16	US-10-466-258-11	Sequence 11, Appl
26	827.7	44.7	776	12	US-10-660-946-5	Sequence 5, Appli
27	827.7	44.7	776	12	US-10-267-502-430	Sequence 430, App
28	825.8	44.6	780	12	US-10-267-502-432	Sequence 432, App
29	818.1	44.2	777	14	US-10-205-219-93	Sequence 93, Appl
30	789.8	42.7	356	12	US-10-660-946-6	Sequence 6, Appli
31	684.2	37.0	208	12	US-10-660-946-7	Sequence 7, Appli
32	682.6	36.9	593	15	US-10-108-260A-2892	Sequence 2892, Ap
33	666.8	36.0	266	12	US-10-276-774-2330	Sequence 2330, Ap
34	666	36.0	267	12	US-10-660-946-8	Sequence 8, Appli
35	666	36.0	267	14	US-10-205-194-127	Sequence 127, App
36	662.6	35.8	269	14	US-10-106-698-6222	Sequence 6222, Ap
37	644.2	34.8	236	9	US-09-729-674-20	Sequence 20, Appl
38	644.2	34.8	236	9	US-09-765-205-26	Sequence 26, Appl
39	644.2	34.8	236	12	US-10-408-967-2	Sequence 2, Appli
40	541.9	29.3	168	10	US-09-809-391-563	Sequence 563, App
41	541.9	29.3	168	10	US-09-882-171-563	Sequence 563, App
42	541.9	29.3	168	12	US-10-164-861-563	Sequence 563, App
43	538.3	29.1	241	12	US-10-660-946-3	Sequence 3, Appli
44	527.9	28.5	222	12	US-10-267-502-428	Sequence 428, App
45	517.4	28.0	234	12	US-10-424-599-200840	Sequence 200840,

ALIGNMENTS

RESULT 1

US-09-789-386-6

; Sequence 6, Application US/09789386

; Patent No. US20020010324A1

; GENERAL INFORMATION:

; APPLICANT: MICHALOVICH, DAVID


```
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1458.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: human
US-09-765-205-6
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Query Match          99.1%; Score 1833.8; DB 9; Length 373;
Best Local Similarity 96.5%; Pred. No. 8.6e-60;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
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Db      301 KFAVLMWVFTTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360

Qy      349 IQAKIPGLKRKAE 361
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Db      361 IQAKIPGLKRKAE 373
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RESULT 3

US-09-893-348-24

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; Sequence 24, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
```

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; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-24

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Query Match          99.1%; Score 1833.8; DB 9; Length 373;
Best Local Similarity 96.5%; Pred. No. 8.6e-60;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

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Qy    229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 288
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Qy    289 KFAVLMWVFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    349 IQAKIPGLKRKAE 361
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Db    361 IQAKIPGLKRKAE 373

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RESULT 4
US-10-408-967-8

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; Sequence 8, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
; FILE REFERENCE: 00925
; CURRENT APPLICATION NUMBER: US/10/408,967
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-967-8
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Query Match          99.1%; Score 1833.8; DB 12; Length 373;
Best Local Similarity 96.5%; Pred. No. 8.6e-60;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
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Db      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAVPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120
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Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTS----- 173
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Db    181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240

Qy    229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 288
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 300

Qy    289 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 KFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360

Qy    349 IQAKIPGLKRKAE 361
        ||||||||||||
Db    361 IQAKIPGLKRKAE 373
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RESULT 5
US-10-060-036-72
; Sequence 72, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
```

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; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-72
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Query Match          99.1%; Score 1833.8; DB 14; Length 373;
Best Local Similarity 96.5%; Pred. No. 8.6e-60;
Matches 360; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPSTS----- 173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPSTPAAPKRRG 180

Qy    174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240

Qy    229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDL 288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDL 300

Qy    289 KFAVLMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 KFAVLMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK 360

Qy    349 IQAKIPGLKRKAE 361
          ||||||||||||
Db    361 IQAKIPGLKRKAE 373
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RESULT 6
US-10-466-258-4
; Sequence 4, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
```

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; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-258-4
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Query Match          98.7%; Score 1825.8; DB 16; Length 373;
Best Local Similarity 96.0%; Pred. No. 1.7e-59;
Matches 358; Conservative 1; Mismatches 2; Indels 12; Gaps 1;
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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPCWDPSVSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTS----- 173
      |||||||||||||||:||||||||||||||||||||||||||||||||||
Db    121 SPLSAAAVSPSKLPQDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    174 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 228
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SSGSVVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG 240

Qy    229 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 288
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLDSL 300

Qy    289 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAK 348
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 KFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAK 360

Qy    349 IQAKIPGLKRKAE 361
      ||||||||||||
Db    361 IQAKIPGLKRKAE 373
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RESULT 7
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
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; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2
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Query Match          95.0%; Score 1756.9; DB 9; Length 1192;
Best Local Similarity 30.3%; Pred. No. 4.9e-56;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;
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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
          |||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP 120
          |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPS----- 171
          |||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    172 ----- 171

Db    181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy    172 ----- 171

Db    241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy    172 ----- 171

Db    301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV 360

Qy    172 ----- 171

Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy    172 ----- 171

Db    421 DKKCFADSLEQTNHEKDSESSNDDTSFSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480

Qy    172 ----- 171

Db    481 PLLGDPTSENKTDEKKIEEKKAIQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE 540

Qy    172 ----- 171

Db    541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600
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Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIIPDVPQKQDETVMVLKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETTFSDSSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV SALAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 8

US-09-758-140-6

; Sequence 6, Application US/09758140

; Patent No. US20020012965A1

; GENERAL INFORMATION:

; APPLICANT: Strittmatter, Stephen M.

; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth

; FILE REFERENCE: 44574-5073-US

; CURRENT APPLICATION NUMBER: US/09/758,140

; CURRENT FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: US 60/175,707

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: US 60/207,366

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 60/236,378

; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6

Query Match 95.0%; Score 1756.9; DB 9; Length 1192;
Best Local Similarity 30.3%; Pred. No. 4.9e-56;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy	1	MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSVTPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSVTPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFVSVPKAESAVIVANPREELIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLLVAAQDSETDYVTTDNLTQVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660

Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV SALAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 9

US-09-893-348-23

; Sequence 23, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-23

Query Match 95.0%; Score 1756.9; DB 9; Length 1192;
Best Local Similarity 30.3%; Pred. No. 4.9e-56;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPS----- 171
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    172 ----- 171

Db    181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPNTISAGQEDFPSVLLETAASLPSLSP 240

Qy    172 ----- 171

Db    241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy    172 ----- 171

Db    301 GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV 360

Qy    172 ----- 171

Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy    172 ----- 171

Db    421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480

Qy    172 ----- 171

Db    481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE 540

Qy    172 ----- 171

Db    541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSF 600

Qy    172 ----- 171
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Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETETSDSSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV SALAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALENGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALENGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 10

US-09-972-599A-6

; Sequence 6, Application US/09972599A

; Patent No. US20020077295A1

; GENERAL INFORMATION:

; APPLICANT: STRITTMATTER, STEPHEN M.

; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

; FILE REFERENCE: C077 CIP US

; CURRENT APPLICATION NUMBER: US/09/972,599A

; CURRENT FILING DATE: 2001-10-06

; PRIOR APPLICATION NUMBER: PCT/US01/01041

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 09/758,140

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 60/236,378

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/207,366

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

Query Match 95.0%; Score 1756.9; DB 9; Length 1192;
Best Local Similarity 30.3%; Pred. No. 4.9e-56;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy	1	MEDLDQSPVLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPVLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVLVAAQDSETDYVTTDNLTQVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	660

Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMMLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLLPPDVSA LAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 11

US-10-267-502-429
; Sequence 429, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-429

Query Match 95.0%; Score 1756.9; DB 12; Length 1192;
 Best Local Similarity 30.3%; Pred. No. 4.9e-56;
 Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLKESLTETSFESMI	780
Qy	172	-----	171

Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840

Qy 172 ----- 171

Db 841 SNDDLFIKSEAQIRETETETFSDDSSPIEIIIDEFPTLISSKTDSDFSKLAREYTDLEVSHKSEI 900

Qy 172 ----- 171

Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALAT 960

Qy 172 -----TSVVDLLYWRDIKKTGVV 189
 |||

Db 961 QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020

Qy 190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE 249
 |||

Db 1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE 1080

Qy 250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL 309
 |||

Db 1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL 1140

Qy 310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 |||

Db 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 12

US-10-060-036-71

; Sequence 71, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Heppler, William T.

; APPLICANT: Jiang, Yuqiu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

; FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

; CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 71

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-060-036-71

Query Match 95.0%; Score 1756.9; DB 14; Length 1192;

Best Local Similarity 30.3%; Pred. No. 4.9e-56;

Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy 1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171

```

Db      841 SNDDLFIKSEAQIRETETFSDDSSPIEIIIDFPTLISSKTD SFSKLAREYTDLEVSHKSEI 900
Qy      172 ----- 171
Db      901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV SALAT 960
Qy      172 -----TSVVDLLYWRDIKKTGVV 189
          |||
Db      961 QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020
          |||
Qy      190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE 249
          |||
Db      1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE 1080
          |||
Qy      250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVAVLMWVFTYVGALFNGLT L 309
          |||
Db      1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVAVLMWVFTYVGALFNGLT L 1140
          |||
Qy      310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
          |||
Db      1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192
          |||

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RESULT 13

US-10-327-213-9

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; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
; APPLICANT: FILBIN, MARIE T.
; APPLICANT: DOMENICONI, MARCO
; APPLICANT: CAO, ZIXUAN
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
; FILE REFERENCE: CUNY/003
; CURRENT APPLICATION NUMBER: US/10/327,213
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-327-213-9

```

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Query Match          95.0%; Score 1756.9; DB 16; Length 1192;
Best Local Similarity 30.3%; Pred. No. 4.9e-56;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

```

```

Qy      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
          |||
Db      1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
          |||
Qy      61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
          |||
Db      61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
          |||
Qy      121 SPLSAAVSPSKLPEDDEPPARPPPPASVSPQAEVWTPPAPAPAAPP----- 171

```

Db	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETFSDDSPIEIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPPDVSALAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189


```

Db      961 QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV 1020
Qy      190 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESE 249
        |||
Db      1021 FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESE 1080
Qy      250 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVDLKFVAVLMWVFTYVGFALFNGLTTL 309
        |||
Db      1081 VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVDLKFVAVLMWVFTYVGFALFNGLTTL 1140
Qy      310 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
        |||
Db      1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

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RESULT 14

US-10-466-258-9

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; Sequence 9, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: ASSAY
; FILE REFERENCE: P80966 GCW
; CURRENT APPLICATION NUMBER: US/10/466,258
; CURRENT FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-466-258-9

```

```

Query Match          95.0%; Score 1756.9; DB 16; Length 1192;
Best Local Similarity 30.3%; Pred. No. 4.9e-56;
Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

```

```

Qy      1 MEDLDQSPVLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
        |||
Db      1 MEDLDQSPVLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
Qy      61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP 120
        |||
Db      61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP 120
Qy      121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPS----- 171
        |||
Db      121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180
Qy      172 ----- 171
Db      181 SSGSVDETLEFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240
Qy      172 ----- 171
Db      241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

```

Qy	172	-----	171
Db	301	GSSFVSVPKASAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPSTENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLPPDVSALAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361

Db 1141 LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 15

US-10-408-967-7

; Sequence 7, Application US/10408967
; Publication No. US20040063161A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Yan, Riqiang
; APPLICANT: Lu, Yifeng
; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
; FILE REFERENCE: 00925
; CURRENT APPLICATION NUMBER: US/10/408,967
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-967-7

Query Match 94.6%; Score 1749.9; DB 12; Length 1192;
Best Local Similarity 30.2%; Pred. No. 8.9e-56;
Matches 360; Conservative 0; Mismatches 1; Indels 831; Gaps 1;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
|
Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
|
Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

Qy 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPS----- 171
|
Db 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG 180

Qy 172 ----- 171

Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy 172 ----- 171

Db 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy 172 ----- 171

Db 301 GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV 360

Qy 172 ----- 171

Db 361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy 172 ----- 171

Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPSTENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLINTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA LAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFPAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRRLFLVDDLVDLSLKFAVLMWVFTYVGALENGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRRLFLVDDLVDLSLKFAVLMWVFTYVGALENGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

Search completed: September 29, 2004, 19:11:36
 Job time : 93.1193 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:40:14 ; Search time 76.6061 Seconds
(without alignments)
1486.854 Million cell updates/sec

Title: SEQ29_1-172_990-1178
Perfect score: 1850
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length DB	ID			Description

1	1833.9	99.1	392	4	Q96B16	Q96b16 homo sapien
2	1533	82.9	375	11	Q8BHF5	Q8bhf5 mus musculu
3	1523.1	82.3	356	11	Q8BH78	Q8bh78 mus musculu
4	1513	81.8	357	11	Q8K3G7	Q8k3g7 mus musculu
5	1455.3	78.7	1162	11	Q8BGM9	Q8bgm9 mus musculu
6	1441.2	77.9	1163	11	Q8K3G8	Q8k3g8 mus musculu
7	1028	55.6	986	4	Q8IUA4	Q8iua4 homo sapien
8	994	53.7	1046	11	Q8BGK7	Q8bgk7 mus musculu
9	989.2	53.5	639	11	Q8K290	Q8k290 mus musculu
10	986.8	53.3	578	11	Q80W95	Q80w95 mus musculu
11	901	48.7	184	6	Q7YRW9	Q7yrw9 bos taurus
12	883.2	47.7	199	13	Q7T224	Q7t224 gallus gall
13	867	46.9	179	6	Q9GM33	Q9gm33 macaca fasc
14	829.8	44.9	780	11	Q8K0T0	Q8k0t0 mus musculu
15	825.8	44.6	780	11	Q8K4S4	Q8k4s4 mus musculu
16	793.3	42.9	760	13	Q90638	Q90638 gallus gall
17	750.9	40.6	214	13	Q7T222	Q7t222 carassius a
18	705.1	38.1	643	11	Q8CCU2	Q8ccu2 mus musculu
19	683	36.9	199	4	Q9BQ59	Q9bq59 homo sapien
20	673.3	36.4	720	11	Q7TNB7	Q7tnb7 mus musculu
21	669.9	36.2	208	13	Q90637	Q90637 gallus gall
22	669.2	36.2	595	5	Q9VMV9	Q9vmv9 drosophila
23	666	36.0	267	11	Q63765	Q63765 rattus sp.
24	652.4	35.3	236	11	Q8VBU0	Q8vbu0 rattus norv
25	651.1	35.2	237	11	Q8C6D5	Q8c6d5 mus musculu
26	595.6	32.2	221	13	Q7ZUD6	Q7zud6 brachydanio
27	529.3	28.6	234	5	Q9VMW3	Q9vmw3 drosophila
28	527.9	28.5	222	5	Q9VMW4	Q9vmw4 drosophila
29	521	28.2	224	5	Q9VMW1	Q9vmw1 drosophila
30	518	28.0	202	5	Q9VMW2	Q9vmw2 drosophila
31	454.3	24.6	2484	5	Q9U347	Q9u347 caenorhabdi
32	447	24.2	2607	5	Q23187	Q23187 caenorhabdi
33	353.5	19.1	222	5	Q23188	Q23188 caenorhabdi
34	343	18.5	107	13	Q7T223	Q7t223 carassius a
35	286.7	15.5	1179	12	Q91L98	Q91l98 white spot
36	286.6	15.5	1180	12	Q8VAS9	Q8vas9 white spot
37	286.1	15.5	1185	12	Q8QTC5	Q8qtc5 white spot
38	277	15.0	1312	4	Q9NR59	Q9nr59 homo sapien
39	277	15.0	1312	4	Q7Z5V7	Q7z5v7 homo sapien
40	277	15.0	1343	4	Q9H7N4	Q9h7n4 homo sapien
41	277	15.0	1627	10	Q84ZL0	Q84zl0 oryza sativ
42	275.1	14.9	1173	11	Q63624	Q63624 rattus norv
43	267.3	14.4	2301	10	Q9ATK5	Q9atk5 chlamydomon
44	266.4	14.4	1049	5	Q8MRP5	Q8mrp5 drosophila
45	266.4	14.4	1154	5	Q8IQ12	Q8iq12 drosophila

ALIGNMENTS

RESULT 1

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.

AC Q96B16;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)


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Qy      173 -----SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVT 209
          : |||||
Db      181 SSGSVDETLFALPAASEPVIRSSAVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVT 240

Qy      210 AYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVN 269
          |||||
Db      241 AYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVN 300

Qy      270 CTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQA 329
          |||||
Db      301 CTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQA 360

Qy      330 QIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
          |||||
Db      361 QIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 392

```

RESULT 2

Q8BHF5

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ID  Q8BHF5          PRELIMINARY;          PRT;    375 AA.
AC  Q8BHF5;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  RTN4.
GN  RTN4.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=129/SvcJ7, and 129SvcJ7;
RA  Oertle T., van der Putten H., Schwab M.E.;
RT  "Genomic Structure and Functional Characterization of the Promoter
RT  Structures of Human and Mouse Nogo/Rtn-4.";
RL  Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=129/SvcJ7, and 129SvcJ7;
RA  Oertle T., Schwab M.E.;
RL  Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=129/SvcJ7;
RA  Van der Putten H.;
RL  Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN  [4]
RP  SEQUENCE FROM N.A.
RC  STRAIN=129SvcJ7;
RA  Van der Putten H., Mir A.;
RL  Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AY102282; AAM73504.1; -.
DR  EMBL; AY102286; AAM73509.1; -.
DR  MGD; MGI:1915835; Rtn4.
DR  GO; GO:0005783; C:endoplasmic reticulum; IDA.

```


Query Match 82.9%; Score 1533; DB 11; Length 375;
Best Local Similarity 82.8%; Pred. No. 1.1e-55;
Matches 317; Conservative 13; Mismatches 23; Indels 30; Gaps 7;

Qy	1	MEDLDQSP	LVSSS--DSPPRPQPA	FKYQFVREPEDEE	EEEEEEEEDEDEDLEE	LEVLERKP	59	
Db	1	MEDIDQSS <td>LVSSSADSP <td>PPRPPPAFKYQFVTE <td>PEDEEDEDEDEDEDEDE</td> <td>DEDEDLEE</td> <td>LEVLERKP 60</td> </td></td>	LVSSSADSP <td>PPRPPPAFKYQFVTE <td>PEDEEDEDEDEDEDEDE</td> <td>DEDEDLEE</td> <td>LEVLERKP 60</td> </td>	PPRPPPAFKYQFVTE <td>PEDEEDEDEDEDEDEDE</td> <td>DEDEDLEE</td> <td>LEVLERKP 60</td>	PEDEEDEDEDEDEDEDE	DEDEDLEE	LEVLERKP 60	
Qy	60	AAGLSAAP <td>VPTAPAA <td>AGAPLMDFGNDFVPP <td>PAPRGPLPAAP <td>PPVAPERQPSWD</td> <td>PSPVSSTVPA 119</td> </td></td></td>	VPTAPAA <td>AGAPLMDFGNDFVPP <td>PAPRGPLPAAP <td>PPVAPERQPSWD</td> <td>PSPVSSTVPA 119</td> </td></td>	AGAPLMDFGNDFVPP <td>PAPRGPLPAAP <td>PPVAPERQPSWD</td> <td>PSPVSSTVPA 119</td> </td>	PAPRGPLPAAP <td>PPVAPERQPSWD</td> <td>PSPVSSTVPA 119</td>	PPVAPERQPSWD	PSPVSSTVPA 119	
Db	61	AAGLSAAP <td>VPP--PAA-AP <td>LLDFSSDSVPP <td>PAPRGPLPAAP</td> <td>PPTAPERQPSWERS</td> <td>PAAS---A 114</td> </td></td>	VPP--PAA-AP <td>LLDFSSDSVPP <td>PAPRGPLPAAP</td> <td>PPTAPERQPSWERS</td> <td>PAAS---A 114</td> </td>	LLDFSSDSVPP <td>PAPRGPLPAAP</td> <td>PPTAPERQPSWERS</td> <td>PAAS---A 114</td>	PAPRGPLPAAP	PPTAPERQPSWERS	PAAS---A 114	
Qy	120	PSPLSAAA <td>VSPSKLPEDDEPP <td>PARPPPPPPASV <td>SPQAEPVWT</td> <td>PPAPA-----</td> <td>165</td> </td></td>	VSPSKLPEDDEPP <td>PARPPPPPPASV <td>SPQAEPVWT</td> <td>PPAPA-----</td> <td>165</td> </td>	PARPPPPPPASV <td>SPQAEPVWT</td> <td>PPAPA-----</td> <td>165</td>	SPQAEPVWT	PPAPA-----	165	
Db	115	PSLP	PAAVLP <td>SKLPEDDEPP</td> <td>AR--PPAPAGAS</td> <td>PLAEPAAP</td> <td>PSTPAAPKRRGSGSVDETL 172</td>	SKLPEDDEPP	AR--PPAPAGAS	PLAEPAAP	PSTPAAPKRRGSGSVDETL 172	
Qy	166	---	PAAP----	PSTSVVDLL	YWRDIKKTGV	VFGASLFL	LLSLTVFSIVSVTAYIALALLS 218	
Db	173	FAL	PAASEP	VIPSSAVVDLL	YWRDIKKTGV	VFGASLFL	LLSLTVFSIVSVTAYIALALLS 232	
Qy	219	VTISFRI	YKGV	IQAIQKSDE	GHPFRAYLE	SEVAISEEL	VQKYSNSALGHVNCTIKELRRL 278	
Db	233	VTISFRI	YKGV	IQAIQKSDE	GHPFRAYLE	SEVAISEEL	VQKYSNSALGHVNSTIKELRRL 292	
Qy	279	FLVDDL	VD	SLKFAVLM	WVFTYV	GALFENGLTLL	LILALISLFSVPVIYERHQAQIDHYLG	338
Db	293	FLVDDL	VD	SLKFAVLM	WVFTYV	GALFENGLTLL	LILALISLFSIPVIYERHQAQIDHYLG	352
Qy	339	NKNV	KDAMAKI	QAKIPGL	KRKAE		361	
Db	353	NKSV	KDAMAKI	QAKIPGL	KRKAE		375	

Q8BH78

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ID      Q8BH78      PRELIMINARY;      PRT;      356 AA.
AC      Q8BH78;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RTN4.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7, and 129SvcJ7;
RA      Oertle T., van der Putten H., Schwab M.E.;
RT      "Genomic Structure and Functional Characterization of the Promoter

```


08K3G7

Query Match 81.8%; Score 1513; DB 11; Length 357;
Best Local Similarity 84.2%; Pred. No. 6.5e-55;
Matches 315; Conservative 11; Mismatches 18; Indels 30; Gaps 8;

Qy	1	MEDLDQSP LVSSS--DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
Db	1	MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEDEDEDEDEDEDEDELEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAGAPLMDFGND FVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVPA	119
Db	61	AAGLSAAPVF--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS---A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTS-----	173
Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	174	-----VVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYK	227
Db	164	GSGSVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYK	223
Qy	228	GVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD	287
Db	224	GVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD	283
Qy	288	LKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMA	347

Db 284 LKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMA 343
 Qy 348 KIQAKIPGLKRKAE 361
 |||||
 Db 344 KIQAKIPGLKRKAE 357

RESULT 5

Q8BGM9

ID Q8BGM9 PRELIMINARY; PRT; 1162 AA.
 AC Q8BGM9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RTN4.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY102284; AAM73506.1; -.
 DR EMBL; AY102286; AAM73511.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 1162 AA; 126613 MW; 855697FBEE11781F CRC64;

Query Match 78.7%; Score 1455.3; DB 11; Length 1162;
 Best Local Similarity 27.3%; Pred. No. 3.5e-51;
 Matches 319; Conservative 11; Mismatches 23; Indels 817; Gaps 8;

Qy 1 MEDLDQSPLVSSS-DSPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKP 59

	: : :	
Db	1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEEEEDDEDLEELEVLERKP	60
Qy	60 AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAFPVAPERQPSWDFSPVSSTVPA	119
	: : :	
Db	61 AAGLSAAPVP--PAA-APLLDFSSDSVPAPRGPLPAAAPTAPERQPSWERSPAAS---A	114
Qy	120 PSPLSAAA VSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTTPAPA-----	165
Db	115 PSLPPAAA VLP SKLPEDDEPPAR--PPAPAGASPLAEPAAPPSTPAAPKRRGSGSVDETL	172
Qy	166 ---PAA-----	168
Db	173 FALPAASEPVIPSSAEKIMDLKEQPGNTVSSSQEDFPSVLFETAASLPSLSPLSTVSFKE	232
Qy	169 -----	168
Db	233 HGYLGNLSAVASTEGTIEETLNEASRELPERATNPFFVNRESAEFSVLEYSEMGSSENGSP	292
Qy	169 -----	168
Db	293 KGESAMLVENTKEEVIVRSKD KEDLVCSAALHNPQESPATLT KVVKEDGVMSPEKTMDIF	352
Qy	169 -----	168
Db	353 NEMKMSVVAPVREEYADF KPFEQAWEVKDTYEGSRDVL AARANMESKV DKKCFEDSLEQK	412
Qy	169 -----	168
Db	413 GHGKDSERENENASFPRTPELVKDGSRAYITCDSFSSATESTAANIFPVLEDHTSENKTD	472
Qy	169 -----	168
Db	473 EKKIEERKAQIITEKTS PKTSNPFLVAIH DSEADYVT T DNLSKVTEAV VATMPEGLTPDL	532
Qy	169 -----	168
Db	533 VQEACESELNEATGTKIAYETKV DLVQTSEAI QESIYPTAQL CPSFEEAEATP SPVLPDI	592
Qy	169 -----PP-----	170
Db	593 VMEAPLN SLLPST GASVAQPSASPLEVPSPVSYDGIKLEPENPPP YEEAMSV ALKTS DSK	652
Qy	171 -----	170
Db	653 EEIKEPESFNAAAQEA EAPYIS IACDLIKETKLSTEP SPEFSNYSEIAKF EKSVPDHCEL	712
Qy	171 -----	170
Db	713 VDDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKKHERLSASPQEV	772
Qy	171 -----	170
Db	773 GKPYLESFQPNL HITKDAASNEIPT LTKKETISLQMEEFN TAIYSND DLLSSKEDKM KES	832
Qy	171 -----	170

Db 833 ETFSDSSPIEIIDEFPTFVSAKDDSPKEYTDLEVS NKSEIANVQSGANSLPCSELPCDLS 892

Qy 171 ----- 170

Db 893 FKNTYPKDEAHVSDEFKSRSSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKLP 952

Qy 171 -----STSVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAY 211
 |||

Db 953 SDTEKEDRSLTAVLSAELNKTSVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAY 1012

Qy 212 IALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCT 271
 |||

Db 1013 IALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNST 1072

Qy 272 IKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQI 331
 |||

Db 1073 IKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQI 1132

Qy 332 DHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 |||:|||||

Db 1133 DHYLGLANKSVKDAMAKIQAKIPGLKRKAE 1162

RESULT 6

Q8K3G8

ID Q8K3G8 PRELIMINARY; PRT; 1163 AA.

AC Q8K3G8;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Nogo-A.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RA Jin W., Long M., Li R., Ju G.;

RT "Cloning and expression of the mouse Nogo-A protein.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY114152; AAM77068.1; -.

DR MGD; MGI:1915835; Rtn4.

DR GO; GO:0005783; C:endoplasmic reticulum; IDA.

DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.

SQ SEQUENCE 1163 AA; 126691 MW; 6B5F362799417EA4 CRC64;

Query Match 77.9%; Score 1441.2; DB 11; Length 1163;

Best Local Similarity 27.2%; Pred. No. 1.4e-50;

Matches 318; Conservative 11; Mismatches 24; Indels 818; Gaps 9;

Qy 1 MEDLDQSPVLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP 59
 |||:||||| ||||| ||||| ||||| |||||:||||:|||||

Db	1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEEEDDEDLEELVLERKP	60
Qy	60 AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPA : : : :	119
Db	61 AAGLSAVPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPTAPERQPSWERSPAAS--A	114
Qy	120 PSPLSAAAVSPSKLPEDDEPPARPPPPPASVSPQAEPVWTTPAPA----- 	165
Db	115 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAAPPSTPAAPKRRGSGSVDETL	172
Qy	166 ---PAA----- 	168
Db	173 FALPAASEPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFFETAASLPSLSPLSTVSFKE	232
Qy	169 -----	168
Db	233 HGYLGNLSAVASTEGETIEETLNEASRELPERATNPFVNRESAEFSVLEYSEMGSSENGSP	292
Qy	169 -----	168
Db	293 KGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTkvVKEDGVMSPEKTMDIF	352
Qy	169 -----	168
Db	353 NEMKMSVVAPVREEYADFkpFEQAWEvKDTYEGSRDVLAAANMESKVdKKCFEDSLEqK	412
Qy	169 -----	168
Db	413 SHGKDSESrNENAsFPSTPeLVkdGsRAYITCDSfTSAtEstAnIFFvLEDHTSenkTD	472
Qy	169 -----	168
Db	473 EKkieERKAQiITEKtSpKtsnPflVAIHdSeAdyvTtDNlSkVTeAvvatmPEGLtpDL	532
Qy	169 -----	168
Db	533 VQEACESELNEATGTkiAYeTKVDLvQtSEAIQESIYPtaQLCPsfEEAEATPspVlpDI	592
Qy	169 -----PP----- 	170
Db	593 VMeaPlNSllPstGasVaQpsASpleVpspvsyDGikLePenppPYeeAMsvAlktSDAK	652
Qy	171 -----	170
Db	653 EEIkEpESFNAAAQEAeApYISIAcdLIketKLStEPSpgfsNYseiAkFEksvpDHCEL	712
Qy	171 -----	170
Db	713 VDDSSPESEPVDLFsDDSIepVpQtQEEavMLmkESltEVsetvtQHkhKERlsASPQEV	772
Qy	171 -----	170
Db	773 GKPyLESfQPNLHiTkDaasNeIPTLtKketISLQMEEfnTAIYSNDdlLsskedKMkes	832
Qy	171 -----	170
Db	833 ETfSDSSPIEIIdEfPtFvSAkDDSPKEYTDleVsNKseIANVQsgANSLPCselPCdLS	892

Qy 171 ----- 170

Db 893 FKNTYPKDEAHVSDEFKSRSSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKLP 952

Qy 171 -----STSVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTA 210
 |||

Db 953 SDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTA 1012

Qy 211 YIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNC 270
 |||

Db 1013 YIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNS 1072

Qy 271 TIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQ 330
 |||

Db 1073 TIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQ 1132

Qy 331 IDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 |||

Db 1133 IDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 1163

RESULT 7

Q8IUA4

ID Q8IUA4 PRELIMINARY; PRT; 986 AA.

AC Q8IUA4;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE RNT4 (RTN4).

GN RTN4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter

RT Structures of Human and Mouse Nogo/Rtn-4.";

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Oertle T., Schwab M.E.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Van der Putten H.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RX MEDLINE=22376540; PubMed=12488097;

RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter

RT Structures of Human and Mouse Nogo/Rtn-4.";

RL J. Mol. Biol. 325:299-323(2003).

Query Match 55.6%; Score 1028; DB 4; Length 986;
Best Local Similarity 39.2%; Pred. No. 1.5e-33;
Matches 250; Conservative 27; Mismatches 60; Indels 300; Gaps 17;

QY	3	DLDQS-----PLVSSSDSPPRP-----QP---	21
		: : :	
Db	372	DLVQTSEVMQESLYPAAQLCPSEFESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSS	431
QY	22	----AFKYQFVR-EPED----EE-----EEEEEEEEDEDEDLEELE-----	53
		: : : : : : : : :	
Db	432	PLEASSVNYESIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISI	491
QY	54	----VLERKPAAGLSAAPVP-----TAPAAGAPLMDFGNDF	85
		: : : : :	
Db	492	ACDLIKETK----LSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDS-EPVDLFSDDS	546
QY	86	VPPAP-----RGPLPAAPP-----	99
		: :	
Db	547	IPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD	606
QY	100	-VAP-----ERQPSWDPSPV-----	113
		: :	
Db	607	TLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDDSSPIEIDEFP	666
QY	114	-----	113
Db	667	TLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI	726
QY	114	-----SSTVPAPSPLSAAA-----VSP-----SKLPEDDEPPARPP	144
		: :	
Db	727	SFSDDFSNGSATS SKVLLLPPDV SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDR--	784
QY	145	PPPPASVSPQAEPVWTPPAPAPAAPSTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS	204
		:	
Db	785	-----SPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS	829
QY	205	IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA	264
Db	830	IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA	889
QY	265	LGHVNCTIKELRRLFLVDDLDVDSLKFVAVLMWVFYVGFALFNGLTLLILALISLFSVPVIY	324
Db	890	LGHVNCTIKELRRLFLVDDLDVDSLKFVAVLMWVFYVGFALFNGLTLLILALISLFSVPVIY	949

Qy 325 ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 |||
 Db 950 ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 986

RESULT 8

Q8BGK7

ID Q8BGK7 PRELIMINARY; PRT; 1046 AA.
 AC Q8BGK7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RTN4.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY102280; AAM73502.1; -.
 DR EMBL; AY102286; AAM73507.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 53.7%; Score 994; DB 11; Length 1046;
 Best Local Similarity 38.6%; Pred. No. 4.7e-32;
 Matches 240; Conservative 31; Mismatches 73; Indels 278; Gaps 15;

Qy 3 DLDQS-----PLVSSSDSPPRP-----QPA-- 22
 |||: |::|||
 Db 440 DLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSAS 499

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Qy      23  -----FKYQFVR-EPEDEEEEEEE-----EEDEDEDLEELE----- 53
          |  :: |||:  ||      :  |  |::|  |
Db      500 PLEVSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAAQAEAPYISI 559

Qy      54  ----VLERKPAAGLSAAPVP-----TAPAAGAPLMDFGND 85
          :  |  |  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      560 ACDLIKETK----LSTEPSPEFSNYSEIAKFEKSVPDHCELVDSSPES-EPVDLFSDDS 614

Qy      86  VPPAPR-----GPLPAAPPVAPERQPSW----- 108
          :|  |:  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      615 IPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASQEVGKPYLESFQPNLHITKDA 674

Qy      109 -----DPSVVSSTVPAPSP 122
          |  ||:  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      675 ASNEIPTLTKKETISLQMEEFNTAIYSNDDLSSKEDMKKESETFSDSSPIEIIDFPTF 734

Qy      123 LSAAAVSP-----SKLPED-----DEPPARPPPPP 147
          :||  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      735 VSAKDDSPKEYTDLEVS NKSEIANVQSGANSLPCSELPCDLSFKNTYPKDE----- 785

Qy      148 PASVSPQAEPVWTPPAPAPAAPPS----- 171
          |  || :  :  :  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      786 -AHVSEFSKSRSSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKLPDTEKEDR 844

Qy      172 -----TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSV 219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      845 SLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSV 904

Qy      220 TISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLF 279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      905 TISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLF 964

Qy      280 LVDDLVDLKFVAVLMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGLAN 339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      965 LVDDLVDLKFVAVLMWVFTYVGALENGLTLLILALISLFSIPVIYERHQAQIDHYLGLAN 1024

Qy      340 KNVKDAMAKIQAKIPGLKRKAE 361
          |:||||||||||||||||||
Db      1025 KSVKDAMAKIQAKIPGLKRKAE 1046

```

RESULT 9

Q8K290

ID Q8K290 PRELIMINARY; PRT; 639 AA.

AC Q8K290;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC032192; AAH32192.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 53.5%; Score 989.2; DB 11; Length 639;
 Best Local Similarity 38.6%; Pred. No. 2.1e-32;
 Matches 240; Conservative 31; Mismatches 73; Indels 278; Gaps 15;

QY	3	DLDQS-----PLVSSSDSPPRP-----QPA--	22
		: :: :	
Db	33	DLVQTSEAIQESIYPTAQLCPSEEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSAS	92
QY	23	-----FKYQFVR-EPEDEEEEEEE-----EEDEDEDLEELE-----	53
		:: : : ::	
Db	93	PLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDAKEEIKEPESFNAAQAEAPYISI	152
QY	54	----VLERKPAAGLSAAPVP-----TAPAAGAPLMDFGNDF	85
		: :: : :	
Db	153	ACDLIKETK----LSTEPSPFEFSNYSEIAKFEKSVPDHCELVDSSPES-EPVDLFSDDS	207
QY	86	VPPAPR-----GPLPAAPPVAPERQPSW-----	108
		: :	
Db	208	IPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA	267
QY	109	-----DPSPVSSSTVPAPSP	122
		: :	
Db	268	ASNEIPTLTKKETISLQMEEFNTAIYSNDDLSSKEDKMKESETFSDSSPIEIIIDFPPTF	327
QY	123	LSAAAVSP-----SKLPED-----DEPPARPPPPP	147
		: :	
Db	328	VSAKDDSPKEYTDLEVS NKSEIANVQSGANSLPCSELPDLSFKNTYPKDE-----	378
QY	148	PASVSPQAEPVWTPPAPAPAAPPS-----	171
		: : : :	
Db	379	-AHVSDEFKSKRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEELPSDTEKEDR	437
QY	172	-----TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSV	219
Db	438	SLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSV	497
QY	220	TISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLF	279
Db	498	TISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLF	557
QY	280	LVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLAN	339
Db	558	LVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLAN	617
QY	340	KNVKDAMAKIQAKIPGLKRKAE	361

Db 618 KSVKDAMAKIQAKIPGLKRKAE 639

RESULT 10

Q80W95

ID Q80W95 PRELIMINARY; PRT; 578 AA.
AC Q80W95;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nogo-A (Fragment).
GN NOGO-A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tozaki H., Hirata T.;
RT "The partial sequence of mouse nogo-A cDNA clone#4109.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB073672; BAC75974.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
FT NON_TER 1 1
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 53.3%; Score 986.8; DB 11; Length 578;
Best Local Similarity 41.1%; Pred. No. 2e-32;
Matches 232; Conservative 21; Mismatches 85; Indels 227; Gaps 8;

Qy 7 SPLVSSSD-----SPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEV---- 54
| | | | | : | : | | | : | |
Db 31 SPLEVPSPVSYDGKLEPENPPPYEEAMSVALKTSDAKEEIKEPESFNAAAQEAAPYIS 90

Qy 55 -----LERKPAAGLS-----AAP-----VPTAPAAGAPLMDFGNDVFPPA 89
| : | | : | : | : | : |
Db 91 IACDLIKETKLSTEPSPGFSNYSEIAKFEKSVDPDHCELVDDSSPESEPVDFLSDDSIPEV 150

Qy 90 PR-----GPLPAAPPVAPERQPSW----- 108
| : | | | : | : | : |
Db 151 PQTQEEAVMLMKESLTVSETVTQHKHKERLSASPQEVGKPYLESFQPNLHITKDAASNE 210

Qy 109 -----DSPVSSTVPAPSPLSAA 126
| | | : | : | : |
Db 211 IPTLTKKETISLQMEEFNTAIYSNDDLSSKEDKMKESETFSDSSPIEIDEFPTFVSAK 270

Qy 127 AVSP----- 130
| |
Db 271 DDSPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDEAHVSDEFKSRSS 330

Qy 131 -----SKLPEDDEPPARPPPPPPASVSPQAE 156
| | | | |
Db 331 VFKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKLPDTEKEDR----- 376

Qy	157	PVWTPPAPAPAAPPSTSVVDLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALAL	216
		:	
Db	377	---SLTAVLSAELNKTSVVDLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALAL	433
Qy	217	LSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELR	276
Db	434	LSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELR	493
Qy	277	RLFLVDDLVDLSLKFAVLMMWFETYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG	336
		:	
Db	494	RLFLVDDLVDLSLKFAVLMMWFETYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLG	553
Qy	337	LANKNVKDAMAKIQAKIPGLKRKAE	361
		:	
Db	554	LANKSVKDAMAKIQAKIPGLKRKAE	578

07YRW9

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ID      Q7YRW9          PRELIMINARY;          PRT;    184 AA.
AC      Q7YRW9;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RTN4w (Fragment).
GN      RTN4.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22715887; PubMed=12832288;
RA      Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT      "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT      RTN/Nogo gene family.";
RL      FASEB J. 17:1238-1247(2003).
DR      EMBL; AY164744; AAP47319.1; -.
FT      NON_TER          1          1
SQ      SEQUENCE    184 AA;  20671 MW;  DE990E03BBAF84A1 CRC64;

```

Query Match 48.7%; Score 901; DB 6; Length 184;
Best Local Similarity 98.9%; Pred. No. 3.9e-30;
Matches 182; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

[illegible]

RESULT 12

07T224

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ID      Q7T224      PRELIMINARY;      PRT;      199 AA.
AC      Q7T224;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RTN4-C.
GN      RTN4.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22715887; PubMed=12832288;
RA      Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT      "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT      RTN/Nogo gene family.";
RL      FASEB J. 17:1238-1247(2003).
DR      EMBL; AY164737; AAP47312.1; -.
SQ      SEQUENCE      199 AA;      22293 MW;      07CF4E4EF2723251 CRC64;

```

Query Match 47.7%; Score 883.2; DB 13; Length 199;
Best Local Similarity 79.2%; Pred. No. 2.7e-29;
Matches 179; Conservative 8; Mismatches 11; Indels 28; Gaps 2;

Qy	136 DDEPPARPPPPPASVSPQAEPVWTPPAPAPAAPPSTSVVDLLLYWRDIKKTGVVFGLSFLF	195
Db	2 DSQP SG-----W-----KDKVVDLLYWRDIKKTGVVFGLSFLF	33
 Qy	196 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE	255
Db	34 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESDDVAIVED	93
 Qy	256 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMMWFVTYVGALFNGLTLILALI	315
Db	94 LIQKYSSVVLGHINGTVKELRRLFLVDDLVDLSLKFAVLMMWFVTYVGALFNGLTLILALI	153
 Qy	316 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAEE	361
Db	154 SLFSVPVIYERHQAQIDHYLGLNKNVKDAMAKIQAKIPGLKRKTE	199

RESULT 13

09GM33

```

ID   Q9GM33          PRELIMINARY;          PRT;   179 AA.
AC   Q9GM33;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)

```

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB049853; BAB16739.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 46.9%; Score 867; DB 6; Length 179;
 Best Local Similarity 98.3%; Pred. No. 9.6e-29;
 Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 183 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHFP 242
 :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIAIQKSDEGHFP 60
 Qy 243 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGA 302
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLREAVLMWVFTYVGA 120
 Qy 303 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179

RESULT 14

Q8K0T0

ID Q8K0T0 PRELIMINARY; PRT; 780 AA.
 AC Q8K0T0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to reticulon 1 (Hypothetical protein).
 GN RTN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;

RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC030455; AAH30455.1; -.
 DR EMBL; BC053926; AAH53926.1; -.
 DR MGD; MGI:1933947; Rtn1.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 780 AA; 83572 MW; 29B47A58FC2F2027 CRC64;

Query Match 44.9%; Score 829.8; DB 11; Length 780;
 Best Local Similarity 28.2%; Pred. No. 1.5e-25;
 Matches 198; Conservative 60; Mismatches 91; Indels 352; Gaps 19;

QY 4 LDQSPL-----VSSSDSPPRPQ---- 20
 || || :||:| | |
 Db 89 LDHSPSSTLKDGEACYSLSIDVCYPPREDSAYFTGILQKENGHITTSSESPEEPETPGP 148
 QY 21 -----PAFKYQFVREPEDEEEEE 37
 | :|| : | : : :
 Db 149 SLPEVPGMEPQGLLSSDSGIEMTPAESTEVNKLADPLDQMKAAYKYIDITRPQEAKGQ 208
 QY 38 EEEEEDEDEDLE----ELEVLERKPAAGLSAAPVPTAPAAG-----APLMD 80
 ||: ||:| | : || : | | : || || | || :|

Db 209 EEQHPGLEDKDLDFKDKDTEVSTK--AEGV-RAPNQAPAVEGKLIKDHLEESTFAPYID 265

Qy 81 FGND-----FVPPAPRGPLPAAPPVAPERQ-----PS----- 107
 :| :| :| :| :|

Db 266 ELSDEQHRVSLVTAPVKITLTEIEPPL----MTATQETIPEKQDLCLKPSPDTPVPTVTVS 321

Qy 108 --WDPSPVSSTVPA----- 119
 | | | | | :

Db 322 EPEDDSPGSVTPPSSGTEPSAAESQGKGSVSEDELIAAIKEAKGLSYETTESPRPVGQVA 381

Qy 120 -----PSPL----- 123
 | | | |

Db 382 DKPKTKTRSGLPPTIPSPLDQEASSAESGDSEIELVSEDPMASEDALPSGYVSFGHVSGPP 441

Qy 124 -----SAAAVSPSKLPEDDEPPARP----- 143
 | : | : | : | : |

Db 442 PSPASPSIQYSILREERAEELDSელი IESCDASSASEESPKR--EQDSPPMKPGALDAIR 499

Qy 144 -----PPP-----PPASVSPQAEP-----VWTPP----- 162
 | | | : : | | |

Db 500 EETGSRATEERAPSHQGPEPDPMLSFAPAAALQSRPEPSSGDGASVPEPPRSQQQKPEE 559

Qy 163 -----APAPAA----PP-----STSVVDLLYWRDIKKTGVVFGASLFLLLSL 200
 | | | : | | | | : | | | : | | |

Db 560 EAVSSSQSPTATEIPGPLGSGLMPPLPFFFNKQKAIDLlyWRDIKQTGIVFGSFLLLFLSL 619

Qy 201 TVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKY 260
 | | : | | | : | | | | | : | : | : | : | : | : |

Db 620 TQFSVVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKY 679

Qy 261 SNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSV 320
 : : : | : | | | | | | | | : | | | | | : : : : : : :

Db 680 TDCLQLYVNSTLKElRRLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLIMAVVSMFTL 739

Qy 321 PVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 | : | : | | : | | | : : : | | | | | | | |

Db 740 PVVYVKHQAQVDQYLGLVRTHINTVVAKIQAKIPGAKRHAE 780

RESULT 15

Q8K4S4

ID Q8K4S4 PRELIMINARY; PRT; 780 AA.

AC Q8K4S4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Reticulon 1A.

GN RTN1 OR RTN-1A.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ICR; TISSUE=Brain;

RA Hirata T., Nomura T., Takagi Y., Sato Y., Tomioka N., Fujisawa H.,

RA Osumi N.;

RT "Mosaic development of the olfactory cortex with Pax6-dependent and -
 RT independent components.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB074899; BAB96551.1; -.
 DR MGD; MGI:1933947; Rtn1.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 780 AA; 83504 MW; 545F5638C576A069 CRC64;

Query Match 44.6%; Score 825.8; DB 11; Length 780;
 Best Local Similarity 28.2%; Pred. No. 2.3e-25;
 Matches 198; Conservative 59; Mismatches 92; Indels 352; Gaps 19;

```

Qy      4 LDQSPL-----VSSSDSPRPQ---- 20
      || ||                      ::||| |
Db      89 LDHSPSSLKDGEGACYTSLISDVCYPPREDSAYFTGILQKENGHITTSESPEEPETPGP 148

Qy      21 -----PAFKYQFVREPEDEEEEE 37
      |:|| : |:::
Db      149 SLPEVPGMEPQGLLSSDSGIEMTPAESTEVNKKILADPLDQMKAEAYKYIDITRPQEAQKQ 208

Qy      38 EEEEEDEDEDLE----ELEVLERKPAAGLSAAPVPTAPAAG-----APLMD 80
      ||: ||:|: || : | |: || || | || :|
Db      209 EEQHPGLEDKDLDFKDKGTEVSTK--AEGV-RAPNQAPAVEGKLIKDHLEFEESTFAPYID 265

Qy      81 FGND-----FVPPAPRGPLPAAPPVAPERQ-----PS----- 107
      :| || : | ||: ||
Db      266 ELSDEQHRVSLVTAPVKITLTEIEPPL---MTATQETIPEKQDLCLKPSPDPTVPTVTVS 321

Qy      108 --WDSPVSSTVPA----- 119
      | || | | | :
Db      322 EPEDDSPGSVTPPSSGTEPSAAESQGKGSVSEDELIAAIKEAKGLSYETTESPRPVGQVA 381

Qy      120 -----PSPL----- 123
      ||||
Db      382 DKPKTKTRSGLPPTIPSPLDQEASSAESGDSEIELVSEDPMASEDALPSGYVSFGHVS GPP 441

Qy      124 -----SAAAVSPSKLPEDDEPPARP----- 143
      ||: || : | | || :|
Db      442 PSPASPSIQYSILREEREAELDSELIIESCDASSASEESPKR--EQDSPMKPGALDAIR 499

Qy      144 -----PPP-----PPASVSPQAEP-----VWTPP----- 162
      | | | |:: : || | ||
Db      500 EETGSRATEERAPSHQGPVEPDMLSFAAAAALQSRPEPSSGDGASVPEPPRSQQQKPEE 559

Qy      163 -----APAPAA----PP-----STSVVDLLYWRDIKKTGVVFGASLFLLLSL 200
      | | || : |||||:|:|:| | || |
Db      560 EAVSSSQSPTATEIPGLGSGLMPPLPFFNKQKAIDL YWRDIKQTGIVFGSFLLLFLSL 619

Qy      201 TVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKY 260
      | ||:| | ||:| | || ||||| |::|:|:|:|:| | : :| :| |
Db      620 TQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKY 679

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Qy 261 SNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSV 320
 :: :|| |:||||||| |||||: |||||:|:|:|:|:
 Db 680 TDCLQLYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLLMVVSMTL 739

Qy 321 PVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 ||:| :|||:| ||| :| :||| || ||
 Db 740 PVVYVKHQAQVDQYLGLVRTHINTVVAKIQAKIPGAKRHAE 780

Search completed: September 29, 2004, 18:54:43
 Job time : 80.6061 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:21:11 ; Search time 15.0208 Seconds
(without alignments)
1251.419 Million cell updates/sec

Title: SEQ29_1-172_990-1178
Perfect score: 1850
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.1

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	%	Length	DB	ID	Description
1	1756.9	95.0	1192	1	RTN4_HUMAN	Q9nqc3	homo sapien
2	1478.8	79.9	1163	1	RTN4_RAT	Q9jkl1	rattus norv
3	911	49.2	199	1	RTN4_MOUSE	Q99p72	mus musculu
4	827.7	44.7	776	1	RTN1_HUMAN	Q16799	homo sapien
5	818.1	44.2	777	1	RTN1_RAT	Q64548	rattus norv
6	651.1	35.2	237	1	RTN3_MOUSE	Q9es97	mus musculu
7	644.2	34.8	236	1	RTN3_HUMAN	O95197	homo sapien
8	592.9	32.0	545	1	RTN2_HUMAN	O75298	homo sapien
9	571.9	30.9	471	1	RTN2_MOUSE	O70622	mus musculu
10	267.4	14.5	555	1	GP1_CHLRE	Q9fpq6	chlamydomon
11	266.4	14.4	1059	1	CAPU_DROME	Q24120	drosophila
12	266	14.4	1206	1	FM14_MOUSE	Q05859	mus musculu
13	266	14.4	1468	1	FMN1_MOUSE	Q05860	mus musculu
14	259.8	14.0	2517	1	NCR2_HUMAN	Q9y618	h nuclear r
15	259.7	14.0	1248	1	DIA1_HUMAN	O60610	homo sapien
16	257.1	13.9	3511	1	MY15_MOUSE	Q9qzz4	mus musculu
17	256.5	13.9	1255	1	DIA1_MOUSE	O08808	mus musculu

18	255.8	13.8	1157	1	BBC1_YEAST	P47068	saccharomyc
19	255.5	13.8	3530	1	MY15_HUMAN	Q9ukn7	homo sapien
20	253.8	13.7	1132	1	BAT3_HUMAN	P46379	homo sapien
21	252.9	13.7	2715	1	MLL4_HUMAN	Q9umn6	homo sapien
22	248.2	13.4	501	1	IRX3_HUMAN	P78415	homo sapien
23	247.3	13.4	980	1	FTKL_DEIRA	Q9rx5	deinococcus
24	247	13.4	2090	1	N214_HUMAN	P35658	homo sapien
25	245.1	13.2	1300	1	SAL3_HUMAN	Q9bxa9	homo sapien
26	244.8	13.2	1375	1	BNR1_YEAST	P40450	saccharomyc
27	244.5	13.2	933	1	PRGR_HUMAN	P06401	homo sapien
28	244	13.2	1790	1	SEPA_EMENI	P78621	emericea
29	243.6	13.2	1719	1	PRD2_HUMAN	Q13029	homo sapien
30	243.3	13.2	786	1	PRGR_CHICK	P07812	gallus gall
31	243.2	13.1	507	1	IRX3_MOUSE	P81067	mus musculu
32	239.2	12.9	449	1	APG_BRANA	P40603	brassica na
33	239.1	12.9	930	1	PRGR_RABIT	P06186	oryctolagus
34	238.3	12.9	3149	1	TEGU_EBV	P03186	epstein-bar
35	236.9	12.8	980	1	RIN3_MOUSE	P59729	mus musculu
36	235.2	12.7	1953	1	BNI1_YEAST	P41832	saccharomyc
37	233.6	12.6	802	1	ENAH_MOUSE	Q03173	mus musculu
38	233.5	12.6	909	1	CNG4_HUMAN	Q14028	homo sapien
39	232.9	12.6	534	1	APG_ARATH	P40602	arabidopsis
40	232.5	12.6	1332	1	M4K6_HUMAN	Q8n4c8	homo sapien
41	231.2	12.5	1567	1	FMN2_MOUSE	Q9j104	mus musculu
42	231.1	12.5	465	1	FXD1_HUMAN	Q16676	homo sapien
43	231.1	12.5	1362	1	BRD4_HUMAN	O60885	homo sapien
44	231	12.5	1164	1	FHOS_HUMAN	Q9y613	homo sapien
45	231	12.5	2774	1	MAPA_RAT	P34926	rattus norv

ALIGNMENTS

RESULT 1

RTN4_HUMAN

ID RTN4_HUMAN STANDARD; PRT; 1192 AA.
AC Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
AC Q9Y5U6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
GN RTN4 OR NOGO OR ASY OR KIAA0886.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129242; PubMed=10667780;
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA Michalovich D., Simmons D.L., Walsh F.S.;
RT "Inhibitor of neurite outgrowth in humans."
RL Nature 403:383-384(2000).
RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=21010696; PubMed=11126360;
 RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
 RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
 RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
 RL Oncogene 19:5736-5746(2000).
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20237542; PubMed=10773680;
 RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
 RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
 RT 2p14-->2p13 by radiation hybrid mapping.";
 RL Cytogenet. Cell Genet. 88:101-102(2000).
 RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 4).
 RA Jin W.-L., Ju G.;
 RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Placenta, and Skeletal muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in human.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [6]

RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fibroblast;
 RA Yutsudo M.;
 RT "Isolation of a cell death-inducing gene.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [7]

RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Pituitary;
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
 RA Luo B., Hu R., Chen J.;
 RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [8]

RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel human cDNA clone with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [9]

RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=99156230; PubMed=10048485;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 5:355-364(1998).
 RN [10]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=20499367; PubMed=11042152;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [12]
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
 RC TISSUE=Brain;
 RA Mao Y.M., Xie Y., Zheng Z.H.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 RN [13]
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Sha J.H., Zhou Z.M., Li J.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [14]
 RP TOPOLOGY.
 RC TISSUE=Brain;
 RX MEDLINE=20129259; PubMed=10667797;
 RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
 RT "Identification of the Nogo inhibitor of axon regeneration as a
 RT Reticulon protein.";
 RL Nature 403:439-444(2000).
 RN [15]
 RP FUNCTION.
 RC TISSUE=Brain;
 RX MEDLINE=21069055; PubMed=11201742;
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

RT regeneration.";
 RL Nature 409:341-346(2001).
 RN [16]
 RP REVIEW.
 RX MEDLINE=21888956; PubMed=11891768;
 RA Ng C.E.L., Tang B.L.;
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 RT regeneration.";
 RL J. Neurosci. Res. 67:559-565(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults.
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-x1 and Bcl-2.
 CC This is likely consecutive to their change in subcellular
 CC location, from the mitochondria to the endoplasmic reticulum,
 CC after binding and sequestration.
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum
 CC through 2 putative transmembrane domains.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
 CC IsoId=Q9NQC3-1; Sequence=Displayed;
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
 CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
 CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
 CC Name=4;
 CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
 CC widely expressed excepted for the liver. Isoform 3 is expressed in
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 CC specific.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to
 CC frameshifts in positions 1149 and 1156.
 CC -----
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 CC -----
 DR EMBL; AJ251383; CAB99248.1; -.
 DR EMBL; AJ251384; CAB99249.1; -.
 DR EMBL; AJ251385; CAB99250.1; -.
 DR EMBL; AB040462; BAB18927.1; -.
 DR EMBL; AB040463; BAB18928.1; -.
 DR EMBL; AF148537; AAG12176.1; -.
 DR EMBL; AF148538; AAG12177.1; -.
 DR EMBL; AF087901; AAG12205.1; -.
 DR EMBL; AF320999; AAG40878.1; -.
 DR EMBL; AF132047; AAD31021.1; -.
 DR EMBL; AF132048; AAD31022.1; -.

DR EMBL; AB015639; BAA83712.1; -.
 DR EMBL; AF077050; AAD27783.1; -.
 DR EMBL; AF177332; AAG17976.1; -.
 DR EMBL; AB020693; BAA74909.1; -.
 DR EMBL; BC001035; AAH01035.1; -.
 DR EMBL; BC007109; AAH07109.1; -.
 DR EMBL; BC014366; AAH14366.1; -.

Query Match 95.0%; Score 1756.9; DB 1; Length 1192;
 Best Local Similarity 30.3%; Pred. No. 2e-50;
 Matches 361; Conservative 0; Mismatches 0; Indels 831; Gaps 1;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPS-----	171
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	172	-----	171
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	172	-----	171
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	172	-----	171
Db	301	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV	360
Qy	172	-----	171
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	172	-----	171
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	172	-----	171
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	172	-----	171
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSP	600
Qy	172	-----	171
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	172	-----	171

Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	172	-----	171
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPOVPQKQDETVMVLKESLTETSFESMI	780
Qy	172	-----	171
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	172	-----	171
Db	841	SNDDLFIKSEAQIRETETFSDDSPIEIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	172	-----	171
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA LAT	960
Qy	172	-----TSVVDLLYWRDIKKTGVV	189
Db	961	QAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVV	1020
Qy	190	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	249
Db	1021	FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESE	1080
Qy	250	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGFALFNGLTL	309
Db	1081	VAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGFALFNGLTL	1140
Qy	310	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	361
Db	1141	LILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 2

RTN4_RAT

ID RTN4_RAT STANDARD; PRT; 1163 AA.

AC Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)

DE (Glut4 vesicle 20 kDa protein).

GN RTN4 OR NOGO.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.

RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;

RX MEDLINE=99249816; PubMed=10231557;

RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;

RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:

RT a new member of the reticulon family.";

RL Biochim. Biophys. Acta 1450:68-76(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20129258; PubMed=10667796;
 RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
 RA Spillmann A.A., Christ F., Schwab M.E.;
 RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
 RT antigen for monoclonal antibody IN-1.";
 RL Nature 403:434-439(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
 RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in rat: one of two
 RT minor splice variants.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=22033691; PubMed=12037567;
 RA GrandPre T., Li S., Strittmatter S.M.;
 RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
 RL Nature 417:547-551(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults (By
 CC similarity).
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
 CC membrane of the endoplasmic reticulum through 2 putative
 CC transmembrane domains (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=Nogo-A, NI-220-250;
 CC IsoId=Q9JK11-1; Sequence=Displayed;
 CC Name=2; Synonyms=Nogo-B, Foocen-M1;
 CC IsoId=Q9JK11-2; Sequence=VSP_005658;
 CC Name=3; Synonyms=Nogo-C, VP20;
 CC IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
 CC Name=4; Synonyms=Foocen-M2;
 CC IsoId=Q9JK11-4; Sequence=VSP_005659;
 CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
 CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
 CC present in dorsal root ganglion, sciatic nerve and PC12 cells
 CC after longer exposure. Isoforms 2 and 3 are detected in kidney,
 CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high
 CC level in skeletal muscle. In adult animals isoform 1 is expressed
 CC mainly in the nervous system.
 CC -!- SIMILARITY: Contains 1 reticulon domain.

CC -----
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 CC -----

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DR      EMBL; AF051335; AAF01564.1; -.
DR      EMBL; AJ242961; CAB71027.1; -.
DR      EMBL; AJ242962; CAB71028.1; -.
DR      EMBL; AJ242963; CAB71029.1; -.
DR      EMBL; AF132045; AAD31019.1; -.
DR      EMBL; AF132046; AAD31020.1; -.
DR      GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
DR      GO; GO:0005635; C:nuclear membrane; ISS.
DR      GO; GO:0005515; F:protein binding; ISS.
DR      GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR      GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT      DOMAIN          1      989      CYTOPLASMIC (Potential).
FT      TRANSMEM        990     1010      POTENTIAL.
FT      DOMAIN          1011     1104      LUMENAL (Potential).
FT      TRANSMEM        1105     1125      POTENTIAL.
FT      DOMAIN          1126     1163      CYTOPLASMIC (Potential).
FT      DOMAIN          976     1163      RETICULON.
FT      DOMAIN          33       46      POLY-GLU.
FT      DOMAIN          73       76      POLY-ALA.
FT      DOMAIN          140      145      POLY-PRO.
FT      VARSPLIC        1       964      Missing (in isoform 3).
FT                                     /FTId=VSP_005656.
FT      VARSPLIC        965      975      AVLSAELSKTS -> MDGQKKHWKDK (in isoform
FT                                     3).
FT                                     /FTId=VSP_005657.
FT      VARSPLIC        173      975      Missing (in isoform 2).
FT                                     /FTId=VSP_005658.
FT      VARSPLIC        192      975      Missing (in isoform 4).
FT                                     /FTId=VSP_005659.
FT      CONFLICT        1130     1131      MISSING (IN REF. 3; AAD31020).
SQ      SEQUENCE        1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;

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Qy	1	MEDLDQSPVLVSSS--DSPPRPQPAFKYQFVREPEDEE-----EEEEEEEEDEDEDLEELEVLERK	58
Db	1	MEDIDQSSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELEVLERK	60
Qy	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVP	118
Db	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
Qy	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPA-----	165
Db	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPSTPAAPKRRGSGSVDET	175
Qy	166	----PAA-----	168
Db	176	LFALPAASEPVI PSSAEKIMDLMEQP GNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFK	235
Qy	169	-----	168

Db	236	EHGYLGNL SAVSSSEG TIEETLNEASKELPERATNP FVNRDLAEFSELEYSEMGSSFKGS	295
Qy	169	-----	168
Db	296	PKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQ	355
Qy	169	-----	168
Db	356	MSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED SLEQKSLGK	415
Qy	169	-----	168
Db	416	DSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFP LLEDHTSENKTDEKKI	475
Qy	169	-----	168
Db	476	EERKAQIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEA	535
Qy	169	-----	168
Db	536	CESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEA	595
Qy	169	-----PP-----	170
Db	596	PLNSLLPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTKEGIK	655
Qy	171	-----	170
Db	656	EPESFNAAVQETEAPYIS IACDLIKETKLSTEPSPDFS NYSEIAKFEKSVPEHAELVEDS	715
Qy	171	-----	170
Db	716	SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESL TEVSETVAQHKEERLSASPQELGKPYL	775
Qy	171	-----	170
Db	776	ESFQPNLHSTKDAASNDIPTLT KKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSD	835
Qy	171	-----	170
Db	836	SSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFK	895
Qy	171	-----	170
Db	896	NIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSD	955
Qy	171	-----STSVVDLLYWRDIKKTGVVFGASL FLLL S LTVFSIVSVTAYIA	213
Db	956	TEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASL FLLL S LTVFSIVSVTAYIA	1015
Qy	214	LALLSVTISFRIYKGV I QAIQKSDEGHPFRAYLESEVAI SEELVQKYSNSALGHVNCTIK	273
Db	1016	LALLSVTISFRIYKGV I QAIQKSDEGHPFRAYLESEVAI SEELVQKYSNSALGHVNSTIK	1075
Qy	274	ELRRLFLVDDLVDLSLKFVLMWVFTYV GALFNGLTLLILALISLFSVPVIYERHQ AQIDH	333
		:	

Db 1076 ELRRFLVDDLVDLSKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDH 1135

Qy 334 YLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 |||||:|||||||:

Db 1136 YLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

RESULT 3

RTN4_MOUSE

ID RTN4_MOUSE STANDARD; PRT; 199 AA.

AC Q99P72; Q9CTE3;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).

GN RTN4 OR NOGO.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3T3-L1; TISSUE=Adipocyte;

RA Coulson A.C., Craggs P.D., Morris N.J.;

RT "Mouse vp20/RTN4C cDNA.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 170-199 FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help

CC block the regeneration of the nervous central system in adults (By

CC similarity).

CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By

CC similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the

CC membrane of the endoplasmic reticulum through 2 putative

```

CC      transmembrane domains (By similarity).
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=1;
CC          Comment=A number of isoforms may be produced;
CC          Name=1;
CC          IsoId=Q99P72-1; Sequence=Displayed;
CC      -!- SIMILARITY: Contains 1 reticulon domain.
CC      -----
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CC      -----
DR      EMBL; AF326337; AAK08076.1; -.
DR      EMBL; AK003859; -; NOT_ANNOTATED_CDS.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
DR      GO; GO:0005635; C:nuclear membrane; ISS.
DR      GO; GO:0005515; F:protein binding; ISS.
DR      GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR      GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR      GO; GO:0007399; P:neurogenesis; IDA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT      DOMAIN      1      25      CYTOPLASMIC (Potential).
FT      TRANSMEM      26      50      POTENTIAL.
FT      DOMAIN      51      137      LUMENAL (Potential).
FT      TRANSMEM      138      162      POTENTIAL.
FT      DOMAIN      163      199      CYTOPLASMIC (Potential).
FT      DOMAIN      12      199      RETICULON.
SQ      SEQUENCE      199 AA; 22466 MW; 07BE5D580059ED9C CRC64;

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Query Match          49.2%; Score 911; DB 1; Length 199;
Best Local Similarity 98.4%; Pred. No. 4.3e-24;
Matches 185; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      174 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 233
          |||
Db      12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAI 71

Qy      234 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVL 293
          |||
Db      72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVL 131

Qy      294 MWVFTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 353
          |||
Db      132 MWVFTYVGALFENGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKI 191

Qy      354 PGLKRKAE 361
          |||
Db      192 PGLKRKAE 199

```


RESULT 4

RTN1_HUMAN

ID RTN1_HUMAN STANDARD; PRT; 776 AA.
AC Q16799; Q16800; Q16801;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Reticulon 1 (Neuroendocrine-specific protein).
GN RTN1 OR NSP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).
RC TISSUE=Lung carcinoma;
RX MEDLINE=93293865; PubMed=7685762;
RA Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,
RA Ramaekers F.C.S., Van de Ven W.J.M.;
RT "Cloning and expression of alternative transcripts of a novel
RT neuroendocrine-specific gene and identification of its 135-kDa
RT translational product.";
RL J. Biol. Chem. 268:13439-13447(1993).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=96429995; PubMed=8833145;
RA Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,
RA Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;
RT "Genomic organization of the human NSP gene, prototype of a novel gene
RT family encoding reticulons.";
RL Genomics 32:191-199(1996).
RN [3]
RP TISSUE SPECIFICITY.
RX MEDLINE=98228245; PubMed=9560466;
RA Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,
RA Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;
RT "Neuronal differentiation is accompanied by NSP-C expression.";
RL Cell Tissue Res. 292:229-237(1998).
CC -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC membrane trafficking in neuroendocrine cells.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=RTN1-A; Synonyms=NSP-A;
CC IsoId=Q16799-1; Sequence=Displayed;
CC Name=RTN1-B; Synonyms=NSP-B;
CC IsoId=Q16799-2; Sequence=VSP_005644;
CC Name=RTN1-C; Synonyms=NSP-C;
CC IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
CC -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----

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 CC -----

DR EMBL; L10333; AAA59950.1; -.
 DR EMBL; L10334; AAA59951.1; -.
 DR EMBL; L10335; AAA59952.1; -.
 DR PIR; A46583; A46583.
 DR PIR; I60904; I60904.
 DR Genew; HGNC:10467; RTN1.
 DR MIM; 600865; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.
 DR GO; GO:0004871; F:signal transducer activity; NAS.
 DR GO; GO:0030182; P:neuron differentiation; TAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
 KW Phosphorylation.
 FT TRANSMEM 603 623 POTENTIAL.
 FT TRANSMEM 726 746 POTENTIAL.
 FT DOMAIN 589 776 RETICULON.
 FT DOMAIN 609 612 POLY-LEU.
 FT VARSPLIC 1 420 Missing (in isoform RTN1-B).
 FT /FTId=VSP_005644.
 FT VARSPLIC 1 568 Missing (in isoform RTN1-C).
 FT /FTId=VSP_005645.
 FT VARSPLIC 569 588 GPGPLGPGAPPPLLEFLNKQK -> MQATADSTKMDCVWSNW
 FT KSQ (in isoform RTN1-C).
 FT /FTId=VSP_005646.
 SQ SEQUENCE 776 AA; 83617 MW; CA5B6232353096FE CRC64;

Query Match 44.7%; Score 827.7; DB 1; Length 776;
 Best Local Similarity 27.1%; Pred. No. 6.8e-20;
 Matches 196; Conservative 55; Mismatches 89; Indels 383; Gaps 17;

Qy 6 QSPL----- 9
 |||:
 Db 70 QSPVAMETASTGVAGVSSAMDHTFSTTSKDGEGSCYTSLSIDICYPPQEDSTYFTGILQK 129
 Qy 10 ----VSSSDSPPR---PQP----- 21
 |:|:| | |
 Db 130 ENGHVTISESPEELGTPGSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQM 189
 Qy 22 ---AFKYQFVREPEDEEEEEEEEEDEDEDLE----- 50
 |:| : ||: : |: | ||:|:
 Db 190 KAEAYKYIDITRPEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDKPAPVEGKI 249
 Qy 51 -----ELE----- 53
 |:|
 Db 250 IKDHLLEESTFAPYIDDLSEEQRRAPQITTPVKITLTEIEPSVETTTQEKTPEKQDICK 309

QY 54 -----VLERKPAAGLS-- 64
: | | | |
Db 310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQKGKGSISEDELITAIKEAKGLSYE 369
QY 65 ----AAPV-----PTAPAAAGAPL----- 78
| | | | : | |
Db 370 TAENPRPVGQLADRPEVKARSGPPTIP---SPLDHEASSAESGDSEIELVSEDPMMAAEDA 426
QY 79 -----MDFGNDFVPPAPRGPLPAAPPV-----APE 103
: | | : | | | | : : | |
Db 427 LPSGVVSFGHVGPPP----PSPASPSIQYSILREEREAEELDSELIIESCDASSASEESPK 482
QY 104 RQ---PSWDPSPVS-----STVPAPSPLSAAAVSP 130
| : | | : | | | | |
Db 483 REQDSPPMKPSALDAIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGP----- 534
QY 131 SKLPEDD-----EPPARPPPPPPASVSPQAEFVWTPPAP-APAAPP-----STSVVDLL 178
: | | | | | | | | : | | | | | : | | |
Db 535 -ELPPGDGALEPETPMLPRKPEEDSSSNQSPAATKGPGLGPGAPPPLLLFLNKQKAIDLL 593
QY 179 YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDE 238
| | | | : | | : | | | | | : | | | | : | | | | | : | | : | |
Db 594 YWRDIKQTGIVFGSFLLLSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQKTDE 653
QY 239 GHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFT 298
| | | : | | | : : | | : | | : : : | | : | | | | | : |
Db 654 GHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLT 713
QY 299 YVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKR 358
| | | | | | | | : : : : : : : : : | | | | : : : | | | | |
Db 714 YVGALFNGLTLLLMVAVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKR 773
QY 359 KAE 361
| |
Db 774 HAE 776

RESULT 5

RTN1_RAT

ID RTN1_RAT STANDARD; PRT; 777 AA.
AC Q64548; Q64547;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Reticulon 1 (Neuroendocrine-specific protein) (S-rex).
GN RTN1 OR NSP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
RC STRAIN=Wistar; TISSUE=Brain cortex;
RX MEDLINE=96386034; PubMed=8793864;
RA Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
RA Georgiev G.P., Buchman V.L.;
RT "Intracellular compartmentalization of two differentially spliced s-

```

RT    rex/NSP mRNAs in neurons.";
RL    Mol. Cell. Neurosci. 7:289-303(1996).
CC    -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC        membrane trafficking in neuroendocrine cells.
CC    -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By
CC        similarity).
CC    -!- ALTERNATIVE PRODUCTS:
CC        Event=Alternative splicing; Named isoforms=2;
CC        Name=RTN1-B; Synonyms=S-RexB;
CC        IsoId=Q64548-1; Sequence=Displayed;
CC        Name=RTN1-S; Synonyms=S-RexS;
CC        IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC    -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC        PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC        HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC        EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC        TYPES.
CC    -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC        HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC        DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC        THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXS
CC        DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC        HINDBRAIN.
CC    -!- SIMILARITY: Contains 1 reticulon domain.
CC    -----
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC    between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    -----
DR    EMBL; U17604; AAC53046.1; -.
DR    EMBL; U17603; AAC53045.1; -.
DR    InterPro; IPR003388; Reticulon.
DR    Pfam; PF02453; Reticulon; 1.
DR    PROSITE; PS50845; RETICULON; 1.
KW    Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT    TRANSMEM      604      624      POTENTIAL.
FT    TRANSMEM      727      747      POTENTIAL.
FT    DOMAIN        590      777      RETICULON.
FT    DOMAIN        610      613      POLY-LEU.
FT    VARSPLIC      1        569      Missing (in isoform RTN1-S).
FT                                     /FTId=VSP_005647.
FT    VARSPLIC      570      589      IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
FT                                     KSQ (in isoform RTN1-S).
FT                                     /FTId=VSP_005648.
SQ    SEQUENCE      777 AA;  83001 MW;  AF7479C50F28D0AC CRC64;

Query Match          44.2%;  Score 818.1;  DB 1;  Length 777;
Best Local Similarity 28.2%;  Pred. No. 1.4e-19;
Matches 197;  Conservative 56;  Mismatches 97;  Indels 349;  Gaps 19;

Qy          3  DLDQSP-----LVSSSDSPPRPQPAF----- 23
|           ||           |:|       |||      |:
Db          88  DHSSSPTLKDGEACYSLSIDICYPRED SAYFTGILQKENGHITTS ESPEELGTPGPS 147

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Qy 24 -----KYQFVREPEDEEEEE 38
 Db 148 LPEVPGTEPHGLSSDSGIEMTPAESTEVNKILADPLDQMAEACKYIDITRPQEAKGQE 207
 Qy 39 EEEEEDEDEDLE----ELEVLER-----KPAAG----- 62
 Db 208 EQSPGLEDKDLDFKDKDSEVSTKPEGVHAPNQSPVEGKLIKDNLFEEESTFAPYIDELSD 267
 Qy 63 -----LSAAPVP-TAPAAAGAPLMDFGNDFVP-----PAP----- 90
 Db 268 EQHRMSLVITAPVKITLITEIGPPVMTATHETIPEKQDLCLKPSPDTPVPTVTVSEPEDDSPG 327
 Qy 91 -----R 91
 Db 328 SVTPPSSSGTEPSAAESQGKGSVSEDELIAAIKEAKGLSYETTESPRPVGQAADRPKV KAR 387
 Qy 92 GPLPAAP-----PVAPERQPSWDFSP-----VSSTVPAP 120
 Db 388 SGLPTIPSSLDQEASSAESGDSEIELVSEDPMASE-----DALPSGYVSFGHVSG--PPP 440
 Qy 121 SPL-----SAAAVSPSKLPEDDEPPARP----- 143
 Db 441 SPASPSIQYSILREEREAELDSELIIESCDASSASEESPKR--EQDSPPMKPGVLD AIRE 498
 Qy 144 -----PPPPPASVSP-----QAEPVWTPP----- 162
 Db 499 ETSSRATEERAPSHQGPVEPDPILSFTPVTLQSRPEPSSGDGAPVPEPPKSQQQKPEEEA 558
 Qy 163 ---APAPAA-----PP-----STSVVDLLYWRDIKKTGVVFGASLFLLLSLTV 202
 Db 559 VSSSQSPAATEIPGPLGSDLVPPLPFFFNKQKAIDLLYWRDIKQTGIVFGSFLLLFLSLTQ 618
 Qy 203 FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSN 262
 Db 619 FSVVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTD 678
 Qy 263 SALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPV 322
 Db 679 CLQLYVNSTLKLRLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLLMAVSMFTLPV 738
 Qy 323 IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 361
 Db 739 VYVKHQAQVDQYLGLVLRTHINTVVAKIQAKIPGAKRHAE 777

RESULT 6

RTN3_MOUSE

ID RTN3_MOUSE STANDARD; PRT; 237 AA.

AC Q9ES97;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Reticulon protein 3.

GN RTN3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;
 RT "Cloning and expression profile of a novel mouse cDNA encoding a human
 RT RTN3 homolog.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF195940; AAG31360.1; -.
 DR EMBL; BC014697; AAH14697.1; -.
 DR MGD; MGI:1339970; Rtn3.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 69 89 POTENTIAL.
 FT TRANSMEM 167 187 POTENTIAL.
 FT DOMAIN 49 237 RETICULON.
 SQ SEQUENCE 237 AA; 25428 MW; EB60A0A7AC45F0DE CRC64;

Query Match 35.2%; Score 651.1; DB 1; Length 237;

Best Local Similarity 37.3%; Pred. No. 3.1e-15;
Matches 133; Conservative 40; Mismatches 55; Indels 129; Gaps 4;

Qy	6	QSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSA	65
Db	9	QSPSVSSSSS-----	18
Qy	66	APVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSA	125
Db	19	-----GA-----	27
Qy	126	AAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTSVVDLLYWRDIKK	185
			: : : :
Db	28	GGGSPGA-----	60
		-----CPALGAKSCGSSCAVHDLIFWRDVKK	
Qy	186	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	245
		: : :: : : : : : :	
Db	61	TGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRVYKSVIQAVQKSEEGHPFKAY	120
Qy	246	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	305
		: : : : : : : : : : :	
Db	121	LDVDITLSSEAFHNMYNAAMVHVNKALKLIIRLFLVEDLVDLSKLAVFMWLMTYVGAVFN	180
Qy	306	GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE	361
		: : : : :: : : : :	
Db	181	GITLLILAEELLVFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE	237

RESULT 7

```

RTN3_HUMAN
ID     RTN3_HUMAN          STANDARD;          PRT;          236 AA.
AC     O95197;
DT     16-OCT-2001 (Rel. 40, Created)
DT     16-OCT-2001 (Rel. 40, Last sequence update)
DT     10-OCT-2003 (Rel. 42, Last annotation update)
DE     Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like
DE     protein II) (NSPLII).
GN     RTN3 OR NSPL2.
OS     Homo sapiens (Human).
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX     NCBI_TaxID=9606;
RN     [1]
RP     SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC     TISSUE=Retina;
RX     MEDLINE=99265974; PubMed=10331947;
RA     Moreira E.F., Jaworski C.J., Rodriguez I.R.;
RT     "Cloning of a novel member of the reticulon gene family (RTN3): gene
RT     structure and chromosomal localization to 11q13.";
RL     Genomics 58:73-81(1999).
RN     [2]
RP     SEQUENCE FROM N.A.
RA     Huang X., Zhou Y., Du G., Yuan J., Qiang B.;
RT     "Cloning and expression analysis of a cDNA encoding a novel
RT     neuroendocrine-specific protein-like protein 1: NSPL1.";
RL     Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN     [3]

```

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Eye, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
 CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
 CC RETINA.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF059524; AAC99319.1; -.
 DR EMBL; AF059529; AAD20951.1; -.
 DR EMBL; AF059525; AAD20951.1; JOINED.
 DR EMBL; AF059526; AAD20951.1; JOINED.
 DR EMBL; AF059527; AAD20951.1; JOINED.
 DR EMBL; AF059528; AAD20951.1; JOINED.
 DR EMBL; AF119297; AAD26810.1; -.
 DR EMBL; BC000634; AAH00634.1; -.
 DR EMBL; BC010556; AAH10556.1; -.
 DR EMBL; BC011394; AAH11394.1; -.
 DR EMBL; BC022993; AAH22993.1; -.
 DR Genew; HGNC:10469; RTN3.
 DR MIM; 604249; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 68 88 POTENTIAL.

FT TRANSMEM 177 197 POTENTIAL.
 FT DOMAIN 48 236 RETICULON.
 SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCD7B7 CRC64;

Query Match 34.8%; Score 644.2; DB 1; Length 236;
 Best Local Similarity 54.2%; Pred. No. 5.1e-15;
 Matches 129; Conservative 41; Mismatches 50; Indels 18; Gaps 4;

Qy 138 EPPARPPPPPPASVSPQAEFVWTPPAP----APAAPP-----STSVVDLLYWDRDIK 184
 || | :| | || | || :| | | | :| ||:||||:|
 Db 3 EPSAATQSHSISSSSFGAE----PSAPGGGGSPGACPALGKSCSSSCAVHDLIFWRDVK 58
 Qy 185 KTG VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA 244
 ||| ||| :| :|||| |::|| :| : ||||| ||||| ||||:||||:||||:|
 Db 59 KTG FVFGTTLIMLLSLAAFSVISVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKA 118
 Qy 245 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 304
 ||: :: :| | | :|: | :| : | ||||:||||| || ||: ||||:|
 Db 119 YLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDLSLKLA VFMWLMTYVGAVF 178
 Qy 305 NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 361
 ||:||||| : :||||:||||: ||||:|:| | : ||||:|:| :|:|
 Db 179 NGITLLILAELLIFSVPPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGI AKKAE 236

RESULT 8

RTN2_HUMAN

ID RTN2_HUMAN STANDARD; PRT; 545 AA.
 AC 075298; 060509;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like protein 1) (NSPL1).
 GN RTN2 OR NSPL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RC TISSUE=Lung carcinoma;
 RX MEDLINE=98360096; PubMed=9693037;
 RA Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;
 RT "cDNA cloning, genomic organization, and expression of the human RTN2 gene, a member of a gene family encoding reticulons.";
 RL Genomics 51:98-106(1998).
 RN [2]
 RP SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).
 RC TISSUE=Brain;
 RX MEDLINE=98191726; PubMed=9530622;
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
 RT "Molecular cloning of a novel mouse gene with predominant muscle and neural expression.";
 RL Mamm. Genome 9:274-282(1998).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).

```

CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=RTN2-A;
CC          IsoId=O75298-1; Sequence=Displayed;
CC          Note=Isoform RTN2-C is produced by alternative initiation at
CC          Met-341 of isoform RTN2-A;
CC      Name=RTN2-B;
CC          IsoId=O75298-2; Sequence=VSP_005649;
CC      Event=Alternative initiation;
CC          Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced
CC          by alternative initiation at Met-1 and Met-341;
CC  -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL
CC      MUSCLE.
CC  -!- SIMILARITY: Contains 1 reticulon domain.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF004222; AAC32542.1; -.
DR  EMBL; AF004223; AAC32543.1; -.
DR  EMBL; AF004224; AAC32544.1; -.
DR  EMBL; AF038540; AAC14910.1; -.
DR  Genew; HGNC:10468; RTN2.
DR  MIM; 603183; -.
DR  GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.
DR  GO; GO:0004871; F:signal transducer activity; NAS.
DR  GO; GO:0007165; P:signal transduction; NAS.
DR  InterPro; IPR003388; Reticulon.
DR  Pfam; PF02453; Reticulon; 1.
DR  PROSITE; PS50845; RETICULON; 1.
KW  Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW  Alternative initiation.
FT  CHAIN      1      545      RETICULON PROTEIN 2, ISOFORM RTN2-A.
FT  CHAIN      341     545      RETICULON PROTEIN 2, ISOFORM RTN2-C.
FT  INIT_MET    341     341      FOR ISOFORM RTN2-C.
FT  TRANSMEM    368     388      POTENTIAL.
FT  TRANSMEM    463     483      POTENTIAL.
FT  DOMAIN      345     545      RETICULON.
FT  VARSPLIC    272     344      Missing (in isoform RTN2-B).
FT                                     /FTId=VSP_005649.
SQ  SEQUENCE    545 AA;  59263 MW;  971FD2F909E1E9E6 CRC64;

Query Match          32.0%;  Score 592.9;  DB 1;  Length 545;
Best Local Similarity 27.3%;  Pred. No. 2e-12;
Matches 153;  Conservative 56;  Mismatches 120;  Indels 231;  Gaps 16;

QY      6 QSPLVSSSDSPRPQPAFKYQFVREPEDEE-----EEEEEEEEDEED- 46
      : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     13 EAPSTASS-----TPDSTEGGNDDSDFRELHTAREFSEEDDEEETTSQDW 56

QY     47 -----EDLEELEVLVLE 56
      : | | : |

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Db      57  GTPRELTFSYIAFDGVVSGGRRDSTARRPRPQGRSVSEPRDQHPQPSLGDLSLEIPSL 116
Qy      57  RKPAAGLSAAPVPTAPAAGAPLMD--FGNDFVPPAPRG-----PLPAAPPVA 101
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     117  QSPEPGRRGDP-DTAPPSERPLEDLRLRLDHLGWVARGTGSGEDSSTSSSTPLEDEEPQE 175
Qy     102  PER-----QPSWDP-----SPVSSTVPAPSPLSAAAVSPSKLPEDD 137
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     176  PNRLETGEAGEELDLRLRLAQPS-SPEVLTPQLSPGSGTPQAGTP-----SPSRSRDSN 228
Qy     138  EPPARP-----P 144
      | |
Db     229  SGPEEPLEEKKQWGPLEREPVRGQCLDSTDQLEFTVEPRLLGTAMEWLKTSLLLAVYK 288
Qy     145  PPPPASVSPQAEPVW-----TPP-----APAPAAPSTS-----V 174
      | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     289  TVPILELSP---PLWTAIGWVQRGPTPPTPVLRLVLLKWAKSPRSSGVPSLSLGADMGSKV 345
Qy     175  VDILLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQ 234
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     346  ADILLYWKDTRTSGVVFVTGLMVSLCLLHFSIVSVAHLALLLLCGTISLRVYRKVLQAVH 405
Qy     235  KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFVIM 294
      : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     406  RGDGANPFQAYLDVDLTLTREQTERLSHQITSRVVSAATQLRHFFLVEDLVDSLKLALLF 465
Qy     295  WVFTYVGALFENGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIP 354
      : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     466  YILTFVGAIFENGLTLLILGVIGLFTIPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKIP 525
Qy     355  GL-----KRKAE 361
      | | | |
Db     526  GTGALASAAAASVSGSKAKAE 545

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RESULT 9

RTN2_MOUSE

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ID  RTN2_MOUSE      STANDARD;      PRT;      471 AA.
AC  O70622; O70620;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
DE  protein 1) (NSPLI).
GN  RTN2 OR NSPL1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC  STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;
RX  MEDLINE=98191726; PubMed=9530622;
RA  Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
RT  "Molecular cloning of a novel mouse gene with predominant muscle and
RT  neural expression.";
RL  Mamm. Genome 9:274-282(1998).

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RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RC      TISSUE=Retina;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC      -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
CC          (Potential).
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=2;
CC          Name=1; Synonyms=Brain;
CC              IsoId=O70622-1; Sequence=Displayed;
CC          Name=2; Synonyms=Muscle;
CC              IsoId=O70622-2; Sequence=VSP_005650, VSP_005651;
CC      -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular
CC          tissues.
CC      -!- SIMILARITY: Contains 1 reticulon domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF038537; AAC14906.1; -.
DR      EMBL; AF038537; AAC14907.1; -.
DR      EMBL; AF038538; AAC14908.1; -.
DR      EMBL; AF038539; AAC14909.1; -.
DR      EMBL; AF093624; AAD13195.1; -.
DR      EMBL; BC031370; AAH31370.1; -.
DR      MGD; MGI:107612; Rtn2.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT      TRANSMEM      295      315      POTENTIAL.
FT      DOMAIN        272      471      RETICULON.

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```
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21159092; PubMed=11258910;
RA Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
RA Goodenough U.W.;
RT "Glycosylated polyproline II rods-with-kinks as a structural motif in
RT plant hydroxyproline-rich glycoproteins.";
RL Biochemistry 40:2978-2987(2001).
RN [2]
RP PARTIAL PRELIMINARY SEQUENCE FROM N.A.
RX MEDLINE=91017504; PubMed=1699225;
RA Adair W.S., Apt K.E.;
RT "Cell wall regeneration in Chlamydomonas: accumulation of mRNAs
RT encoding cell wall hydroxyproline-rich glycoproteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
CC -!- FUNCTION: Major component of the outer cell wall W6 (crystalline)
CC layer.
CC -!- SUBUNIT: Associates with GP2 and GP3.
CC -!- PTM: N-glycosylated and O-glycosylated.
```

```

DR      EMBL; AF309494; AAG45420.1; -.
DR      EMBL; M58496; AAA69706.1; ALT_SEQ.
DR      GlycoSuiteDB; Q9FPQ6; -.
DR      InterPro; IPR003882; Pistil_extensin.
DR      PRINTS; PR01218; PSTLEXTENSIN.
KW      Glycoprotein; Repeat; Signal.
FT      SIGNAL          1           29      POTENTIAL.
FT      CHAIN           30          555      VEGETATIVE CELL WALL PROTEIN GP1.
FT      DOMAIN          40          339      49 X 5 AA APPROXIMATE PPSPX REPEATS.
FT      DOMAIN          259         279      POLY-PRO.
FT      CARBOHYD         399         399      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD         455         455      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD         493         493      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE        555 AA;  54219 MW;  6A584A90465502F5 CRC64;

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Qy      7 SPLVSSSDSPPRQPQAFKYQFVREPEDEEEEEEEEEEDEDEDLEELEVLERKPAAGLSAA 66
      :| : | :|| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     143 APPLPPSPAPPSPSP-----PVPPSPSP 165

Qy     67 PVPTAPAAGAPLMDFGNDFVPPAPRGPLPA-----APPVAPERQPSWDPSVPS 114
      ||| :|| :| : ||| :| | | | | | | | | | | | | | | | | | | | | |

```


RL Genes Dev. 9:2482-2494(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -!- SIMILARITY: Contains 1 Formin homology 1 (FH1) domain.
 CC -!- SIMILARITY: Contains 1 Formin homology 2 (FH2) domain.
 CC -!- SIMILARITY: Belongs to the formin homology family. Cappuccino
 CC subfamily.
 CC -----
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 CC -----
 DR EMBL; U34258; AAC46925.1; -.


```

Qy      235 -----KSDEGH----- 240
           || | |
Db      840 QADGFNLDILGKLKDVKSESHNTLLHFIVRTYIAQRRKEGVHPLEIRLPIPEPADVERA 899

Qy      241 -----PFRAYLESEVAISEELVQKYS 261
           ||:::| | ::::|
Db      900 AQMDFEVQQQIFDLNKKFLGCKRRTAKVLAASRPEIMEPFKSKMEEFVEGADKSMAKLH 959

Qy      262 NSALGHVNCTIKELRRLFL-----VDDLVDLSLK 289
           | : | | || | : | | |
Db      960 QS-----LDECRDLFLETMRFYHFSPKACTLTLAQCTPDQFFEYWTNFTNDFKDIWK 1011

Qy      290 FAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAK- 348
           : : | | | : : ||| : : | | : |
Db      1012 -----KEITSLNEL-----MKKSKQAQIE-----SRRNVSTKVEKS 1043

Qy      349 --IQAKIPGLKRKAE 361
           | | | |:::
Db      1044 GRISLKERMLMRRSK 1058

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RESULT 12

FM14_MOUSE

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ID   FM14_MOUSE      STANDARD;          PRT;   1206 AA.
AC   Q05859;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Formin 1 isoform IV (Limb deformity protein).
GN   FMN OR LD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=92112033; PubMed=1339380;
RA   Grusby-Jackson L., Kuo A., Leder P.;
RT   "A variant limb deformity transcript expressed in the embryonic mouse
RT   limb defines a novel formin.";
RL   Genes Dev. 6:29-37(1992).
CC   -!- FUNCTION: Is important in the morphogenesis of limb and may have a
CC       function in differentiated cells or be involved in maintaining
CC       specific differentiated states.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=5;
CC       Comment=Additional isoforms seem to exist;
CC       Name=IV;
CC       IsoId=Q05859-1; Sequence=Displayed;
CC       Name=IA;
CC       IsoId=Q05860-1; Sequence=External;
CC       Name=IB;
CC       IsoId=Q05860-2; Sequence=External;
CC       Name=II;
CC       IsoId=Q05860-3; Sequence=External;

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CC      Name=III;
CC      IsoId=Q05860-4; Sequence=External;
CC      -!- TISSUE SPECIFICITY: It is found throughout the embryo but has a
CC          functional role only in the kidney and limb.
CC      -!- DEVELOPMENTAL STAGE: This is the isoform found in the apical
CC          ectodermal ridge and the mesenchymal compartment of the developing
CC          limb bud.
CC      -!- PTM: PHOSPHORYLATED ON SERINE AND POSSIBLY THREONINE RESIDUES.
CC      -!- SIMILARITY: Contains 1 Formin homology 1 (FH1) domain.
CC      -!- SIMILARITY: Contains 1 Formin homology 2 (FH2) domain.
CC      -!- SIMILARITY: Belongs to the formin homology family. Cappuccino
CC          subfamily.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X62379; CAA44244.1; -.
DR      PIR; S24407; S24407.
DR      MGD; MGI:101815; Fmn.
DR      InterPro; IPR003104; FH2.
DR      InterPro; IPR001265; Formin.
DR      Pfam; PF02181; FH2; 1.
DR      PRINTS; PR00828; FORMIN.
KW      Nuclear protein; Developmental protein; Alternative splicing;
KW      Phosphorylation; Coiled coil.
FT      DOMAIN      418      443      COILED COIL (POTENTIAL).
FT      DOMAIN      497      566      COILED COIL (POTENTIAL).
FT      DOMAIN      644      744      FH1 (PRO-RICH).
FT      DOMAIN      759      1164     FH2.
FT      DOMAIN      1043     1116     COILED COIL (POTENTIAL).
FT      DOMAIN      635      638      POLY-SER.
FT      DOMAIN      751      755      POLY-SER.
SQ      SEQUENCE    1206 AA;  133464 MW;  4DFB38CB52BD8EE7 CRC64;

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Query Match          14.4%;  Score 266;  DB 1;  Length 1206;
Best Local Similarity 17.3%;  Pred. No. 1.1;
Matches 102;  Conservative 40;  Mismatches 97;  Indels 350;  Gaps 24;

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Qy      5  DQSPLVSSSDSPPR-----PQPAFKYQFVREPEDEEE-----EEEE 41
      ||||      :| |      | | |      | ||      : | :
Db      459 DQSPTEQDDRTPGRLQAVWPPPKTK-----DTEEKVGLKYTEAEYQAAILHLKREHK 510

Qy      42 EEDE-----DEDLEEL-EVLERK----- 58
      || |      :| :| | : ||:
Db      511 EEIETLQAQFELKTFHIRGEHALVTARLEEA IENLKQQLKRRREGCEEMRDVCISTDDDC 570

Qy      59 -PAA----- 61
      | |
Db      571 SPKAFRNVCIQTDRETFLKPCDAESKATRSSQIVPKKLTISLTQLSPSKDSKDIHAPFQT 630

Qy      62 --GLSA-----APVPTAPAAGAPLMDFGNDFVPPAP-----RGPLPAAPPVAPERQ 105
      | |:      || || |      ||      :|| |      |||| |||: |

```

```

Db      631 REGTSSSSQKISPPAP-PTPPPLPPPL-----IPPPPLPPGLGPLPPAPPIPP--- 679
Qy      106 PSWDPSPVSSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPA-----SVSPQAE 157
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      680 ----VCPVSPPPPPPPP-----PPTPVPPSDGPPPPPPPPPPPLPNVLALPNSGGPPPPP 729
Qy      158 VWTTPAP--APAAPPSTSV-----VDLLYWRDIKKTGVVFGASLF 195
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      730 PPPPPPPGLAPPPPPGLSFGLSSSSSQYPRKPAIEPSCPMKPLYWTR----- 776
Qy      196 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHP-----FRAY 245
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      777 -----IQINDKSQDAAPTILWDSLEEPHIRDT 802
Qy      246 LESEVAISEELVQ-----KYSNSA--LGHVNCTIKELRR 277
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      803 SEFEYLFKDDTTQKKKKPLSEAYEKKNKVKKIKLLDGKRSQTVGILISLHLEMKDIQQ 862
Qy      278 -LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG 336
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      863 AIFTVDD-----SVVDLETIAALYE----- 882
Qy      337 LANKNVKDAMAKIQ-----AKIPGLKRKAE 361
      | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      883 --NRAQEDELTKIRKYYETSKEEDLKLLDKPEQFLHELAQIPNFAERAQ 929

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RESULT 13

FMN1_MOUSE

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ID   FMN1_MOUSE      STANDARD;          PRT;   1468 AA.
AC   Q05860;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Formin 1 isoforms I/II/III (Limb deformity protein).
GN   FMN OR LD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Testis;
RX   MEDLINE=90363291; PubMed=2392150;
RA   Woychik R.P., Maas R.L., Zeller R., Vogt T.F., Leder P.;
RT   "'Formins': proteins deduced from the alternative transcripts of the
RT   limb deformity gene.";
RL   Nature 346:850-853(1990).
RN   [2]
RP   ALTERNATIVE SPLICING.
RX   MEDLINE=97224459; PubMed=9119367;
RA   Wang C.C., Chan D.C., Leder P.;
RT   "The mouse formin (Fmn) gene: genomic structure, novel exons, and
RT   genetic mapping.";
RL   Genomics 39:303-311(1997).
RN   [3]
RP   PHOSPHORYLATION.

```

RX MEDLINE=93296176; PubMed=8516300;
 RA Vogt T.F., Jackson-Grusby L., Rush J., Leder P.;
 RT "Formins: phosphoprotein isoforms encoded by the mouse limb deformity
 RT locus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5554-5558(1993).
 CC -!- FUNCTION: Is important for the morphogenesis of limb and kidney
 CC and may have a function in differentiated cells or may be involved
 CC in maintaining specific differentiated states.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Comment=Additional isoforms seem to exist;
 CC Name=IA;
 CC IsoId=Q05860-1; Sequence=Displayed;
 CC Name=IB;
 CC IsoId=Q05860-2; Sequence=VSP_001569;
 CC Name=II;
 CC IsoId=Q05860-3; Sequence=VSP_001570;
 CC Name=III;
 CC IsoId=Q05860-4; Sequence=VSP_001571, VSP_001572;
 CC Name=IV;
 CC IsoId=Q05859-1; Sequence=External;
 CC -!- TISSUE SPECIFICITY: It is present in the adult kidney, testis,
 CC limb, ovary, brain, small intestine, salivary gland and harderian
 CC gland. It is present throughout the embryo.
 CC -!- DEVELOPMENTAL STAGE: In the developing limb bud, the protein is
 CC expressed in the apical ectodermal ridge and the mesenchymal
 CC compartment, predominantly in the posterior region. During kidney
 CC morphogenesis, expression is initially restricted to the
 CC epithelial compartment of the pronephros and mesonephros.
 CC -!- PTM: PHOSPHORYLATED ON SERINE AND POSSIBLY THREONINE RESIDUES.
 CC -!- SIMILARITY: Contains 1 Formin homology 1 (FH1) domain.
 CC -!- SIMILARITY: Contains 1 Formin homology 2 (FH2) domain.
 CC -!- SIMILARITY: Belongs to the formin homology family. Cappuccino
 CC subfamily.
 CC -----
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 CC -----
 DR EMBL; X53599; CAA37668.1; -.
 DR PIR; S11515; S11515.
 DR MGD; MGI:101815; Fmn.
 DR InterPro; IPR003104; FH2.
 DR InterPro; IPR001265; Formin.
 DR Pfam; PF02181; FH2; 1.
 DR PRINTS; PR00828; FORMIN.
 DR SMART; SM00498; FH2; 1.
 KW Nuclear protein; Developmental protein; Alternative splicing;
 KW Phosphorylation; Coiled coil.
 FT DOMAIN 723 792 COILED COIL (POTENTIAL).
 FT DOMAIN 870 970 FH1 (PRO-RICH).
 FT DOMAIN 985 1426 FH2.


```
Db      1089 AIFTVDD-----SVVDLETLAALYE----- 1108
Qy      337 LANKNVKDAMAKIQ-----AKIPGLKRKAE 361
        |: :| :||:                |:||   :|:
Db     1109 --NRAQEDELTKIRKYETSKEEDLKLLDKPEQFLHELAOIPNFAERAO 1155
```

NCR2 HUMAN

AC Q9Y618; 000613; 015416; Q13354; Q9Y5U0;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Nuclear receptor co-repressor 2 (N-CoR2) (Silencing mediator of
DE retinoic acid and thyroid hormone receptor) (SMRT) (SMRTe) (Thyroid-,
DE retinoic-acid-receptor-associated co-repressor) (T3 receptor-
DE associating factor) (TRAC) (CTG repeat protein 26).

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

```
RC      TISSUE=Pituitary;
```

RA Ordentlich P., Downes M., Xie W., Genin A., Spinner N.B., Evans R.M.;

Proc. Natl. Acad. Sci. U.S.A. 96:2639-2644 (1999).

RP SEQUENCE FROM N.A. (ISOFORM SMRT).

RX MEDLINE=99199215; PubMed=10097068;

RT "SMRTe, a silencing mediator for retinoid and thyroid hormone

RT receptor corepressor.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:3519-3524 (1999).

RN [3]

RP SEQUENCE OF 1023-2517 FROM N.A.

RC TISSUE=Cervical adenocarcinoma;

RX MEDLINE=96008552; PubMed=7566127;

RA Chen J.D., Evans R.M.;

RT "A transcriptional co-repressor that interacts with nuclear hormone

RT receptors.";

RL Nature 377:454-457 (1995).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM TRAC-1).

RC TISSUE=Fetal liver;

RX MEDLINE=96408715; PubMed=8813722;

RA Sande S., Privalsky M.L.;

RT "Identification of TRACs (T3 receptor-associating cofactors), a family

RT of cofactors that associate with, and modulate the activity of,

RT nuclear hormone receptors.";

RL Mol. Endocrinol. 10:813-825 (1996).

RN [5]

RP SEQUENCE OF 428-613 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=97369492; PubMed=9225980;
 RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.-H., Kidwai A.S.,
 RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;
 RT "cDNAs with long CAG trinucleotide repeats from human brain."
 RL Hum. Genet. 100:114-122(1997).
 RN [6]
 RP INTERACTION WITH MINT.
 RX MEDLINE=21231190; PubMed=11331609;
 RA Shi Y., Downes M., Xie W., Kao H.-Y., Ordentlich P., Tsai C.-C.,
 RA Hon M., Evans R.M.;
 RT "Sharp, an inducible cofactor that integrates nuclear receptor
 RT repression and activation."
 RL Genes Dev. 15:1140-1151(2001).
 RN [7]
 RP INTERACTION WITH HDAC10.
 RX MEDLINE=21839031; PubMed=11739383;
 RA Fischer D.D., Cai R., Bhatia U., Asselbergs F.A.M., Song C., Terry R.,
 RA Trogani N., Widmer R., Atadja P., Cohen D.;
 RT "Isolation and characterization of a novel class II histone
 RT deacetylase, HDAC10."
 RL J. Biol. Chem. 277:6656-6666(2002).
 CC -!- FUNCTION: Mediates the transcriptional repression activity of some
 CC nuclear receptors by promoting chromatin condensation, thus
 CC preventing access of the basal transcription.
 CC -!- SUBUNIT: Interacts with HDAC7 (By similarity). Forms a large
 CC corepressor complex that contains SIN3A/B and histone deacetylases
 CC HDAC1 and HDAC2. This complex associates with the thyroid (TR) and
 CC the retinoid acid receptors (RAR) in the absence of ligand, and
 CC may stabilize their interaction with TFIIB. The SRMT isoform
 CC interacts with HDAC10. Interacts with MINT.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=SMRT; Synonyms=TRAC-2;
 CC IsoId=Q9Y618-1; Sequence=Displayed;
 CC Name=TRAC-1;
 CC IsoId=Q9Y618-2; Sequence=VSP_003412, VSP_003413;
 CC Note=Contains only the C-terminal receptor-interacting domain
 CC and acts as an antirepressor;
 CC -!- TISSUE SPECIFICITY: Ubiquitous. High levels of expression are
 CC detected in lung, spleen and brain.
 CC -!- INDUCTION: Regulated during cell cycle progression.
 CC -!- DOMAIN: The N-terminal region contains repression functions that
 CC are divided into three independent repression domains (RD1, RD2
 CC and RD3). The C-terminal region contains the nuclear receptor-
 CC interacting domains that are divided in two separate interaction
 CC domains (ID1 and ID2).
 CC -!- DOMAIN: The two interaction domains (ID) contain a conserved
 CC sequence referred to as the CORNR box. This motif is required and
 CC sufficient to permit binding to unliganded TR and RARS. Sequences
 CC flanking the CORNR box determine nuclear hormone receptor
 CC specificity.
 CC -!- SIMILARITY: Contains 1 SANT-A domain.
 CC -!- SIMILARITY: Contains 1 Myb-like domain.
 CC -!- SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS


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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF113003; AAD20946.1; -.
DR      EMBL; AF125672; AAD22973.1; -.
DR      EMBL; U37146; AAC50236.1; -.
DR      EMBL; S83390; AAB50847.1; -.
DR      EMBL; U80750; AAB91446.1; -.
DR      PIR; S60255; S60255.
DR      PDB; 1KKQ; 27-FEB-02.
DR      TRANSFAC; T04689; -.
DR      Genew; HGNC:7673; NCOR2.
DR      MIM; 600848; -.
DR      GO; GO:0005634; C:nucleus; TAS.
DR      GO; GO:0003714; F:transcription co-repressor activity; TAS.
DR      InterPro; IPR001005; Myb_DNA_binding.
DR      Pfam; PF00249; myb_DNA-binding; 2.
DR      SMART; SM00717; SANT; 2.
DR      PROSITE; PS50090; MYB_3; 1.
KW      Nuclear protein; Transcription regulation; DNA-binding; Repressor;
KW      Coiled coil; Alternative splicing; 3D-structure.
FT      DOMAIN      174      215      COILED COIL (POTENTIAL).
FT      DOMAIN      254      312      INTERACTION WITH SIN3A/B (BY SIMILARITY).
FT      DNA_BIND     429      474      SANT-A (POTENTIAL).
FT      DNA_BIND     613      657      MYB.
FT      DOMAIN      522      561      COILED COIL (POTENTIAL).
FT      DOMAIN      778      820      PRO-RICH.
FT      DOMAIN      2139     2143     CORNR BOX OF ID1.
FT      DOMAIN      2342     2346     CORNR BOX OF ID2.
FT      DOMAIN      494      510      POLY-GLN.
FT      DOMAIN      682      685      POLY-LYS.
FT      DOMAIN      994      1002     POLY-PRO.
FT      DOMAIN      1384     1389     POLY-PRO.
FT      DOMAIN      1842     1846     POLY-GLY.
FT      DOMAIN      2479     2482     POLY-PRO.
FT      VARSPLIC     1      1702     Missing (in isoform TRAC-1).
FT                                     /FTId=VSP_003412.
FT      VARSPLIC     2353     2398     Missing (in isoform TRAC-1).
FT                                     /FTId=VSP_003413.
FT      CONFLICT      7      7      L -> P (IN REF. 2).
FT      CONFLICT     295     295     K -> E (IN REF. 2).
FT      CONFLICT     309     309     L -> W (IN REF. 2).
FT      CONFLICT     352     352     MISSING (IN REF. 2).
FT      CONFLICT     365     365     A -> P (IN REF. 2).
FT      CONFLICT     612     613     SS -> EF (IN REF. 5).
FT      CONFLICT     711     711     S -> T (IN REF. 2).
FT      CONFLICT     724     740     MISSING (IN REF. 2).
FT      CONFLICT     787     796     RRTSRAPIEP -> PEDIPAPTES (IN REF. 2).
FT      CONFLICT     804     804     G -> L (IN REF. 2).
FT      CONFLICT     814     814     S -> F (IN REF. 2).

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FT CONFLICT 817 817 A -> S (IN REF. 2).
 FT CONFLICT 889 889 G -> R (IN REF. 2).
 FT CONFLICT 1023 1030 SRSPAPPA -> MEAWDAHP (IN REF. 3).
 FT CONFLICT 1034 1034 A -> AEKPVFFPA (IN REF. 2).
 FT CONFLICT 1894 1894 K -> T (IN REF. 4).
 FT CONFLICT 2494 2494 P -> A (IN REF. 4).
 SQ SEQUENCE 2517 AA; 274031 MW; F5805C01761258C0 CRC64;

Query Match 14.0%; Score 259.8; DB 1; Length 2517;
 Best Local Similarity 11.9%; Pred. No. 10;
 Matches 127; Conservative 43; Mismatches 102; Indels 792; Gaps 29;

Qy 6 QSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDL----- 49
 | |: || | : :| | | :| | :| |
 Db 509 QQPM-----PRSSQEEKDEKEKEKEAEKEEEKPEVENDKEDLLKEKTDGDSGEDNDEK 561
 Qy 50 -----EELE 53
 | |:|
 Db 562 EAVASKGRKTANSQGRRKGRITRSMANEANSEEAITPQOSAELASMELNESSRWTEEEEME 621
 Qy 54 VLER----- 57
 ::
 Db 622 TAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQQHKLKMEKERNARR 681
 Qy 58 ----- 57
 Db 682 KKKKAPAAASEEAAFPVVEDEEMEASGVSGNEEEMVEEAALHASGNEVPRGECSGPAT 741
 Qy 58 -----KPAAGLSA-----APVPTAP 72
 | | | | | | :
 Db 742 VNSSDTEIPSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPPRRTSRAPIEPTPASE 801
 Qy 73 AAGAPLMDFGNDFVPPAPRGPLPAAPPVAP-----ERQPSWDPS--- 111
 | | | | | | | | | | :| :|
 Db 802 ATGAPT-----PPPAPPSP-SAPPPVVPKEEKEEETAAAPPVEEGEEQKP---PAAEE 850
 Qy 112 -----PVSSTV----- 117
 | | |
 Db 851 LAVDTGKAEFPVKSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSG 910
 Qy 118 -----PAPSPLS-----A 125
 | | | :|
 Db 911 APQSDSDSATCSADEVDEAEGGDKNRLSPRPSLLTPTGDPRANASPOKPLDLKQLKQRA 970
 Qy 126 AAVSPSKLPEDDEP-----PARPPPPPPASVSPQAE----- 156
 | |: | : : | | | | | | :| :| :| :|
 Db 971 AAIPPIQVTKVHEPPREDAAPTKPAPPAPPPQNLQPESDAPQQPGSSPRGKSRSPAPPA 1030
 Qy 157 -----PVWT-----PPAPAPAA----- 168
 | | | | | :|
 Db 1031 DKEAFAAEAQKLPDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHD 1090
 Qy 169 -----PPSTS-----VV 175
 | |:| :
 Db 1091 TARPVLPRPPTISNPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTM 1150
 Qy 176 DLLYWRDIKKTGVVFGASLFLLLSLTVFSIV-----SVTA 210

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      |   |   |   |   |   |   |   |   |   |
Db    1151 GLPLPMDPKK-----LAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLR 1196
QY    211 YIALALL---SVT-----ISFR-----IYKGVIAI----- 233
      || :   |::|   |::|   :||| | |
Db    1197 GTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRLD 1256
QY    234 -----QKSD-----EG 239
      | |   | |
Db    1257 RGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEG 1316
QY    240 HPFRA-----YLESEVA 251
      ||   | | |
Db    1317 RVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHRGSITQGIPRSYVEAQEDYLRREAK 1376
QY    252 I-----SEELVQKYSNSALGHVN-----CTIKELRRLFLVDDLVDLDFSLKF 290
      :   | : | : | | | :   | : | |
Db    1377 LLKREGTPPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGR----- 1423
QY    291 AVLMMVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVK----- 343
      | : : | | | :   | | | : : |
Db    1424 -----SIHEIPREELRHTPE----LPLAPRPLKEGSITQG 1454
QY    344 -----DAMAKIQA 351
      | | | : |
Db    1455 TPLKYDTGASTTGSKKHDVRSLLIGSPGRTFPPVHPLDVMADARA 1498

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RESULT 15

DIAL_HUMAN

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ID   DIAL_HUMAN          STANDARD;          PRT;   1248 AA.
AC   O60610; Q9UC76;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Diaphanous protein homolog 1 (Diaphanous-related formin 1) (DRF1).
GN   DIAPH1 OR DIAP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98028756; PubMed=9360932;
RA   Lynch E.D., Lee M.K., Morrow J.E., Welcsh P.L., Leon P.E., King M.-C.;
RT   "Nonsyndromic deafness DFNA1 associated with mutation of a human
RT   homolog of the Drosophila gene diaphanous.";
RL   Science 278:1315-1318(1997).
RN   [2]
RP   SEQUENCE OF 218-817 FROM N.A.
RC   TISSUE=Ovarian carcinoma;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

```

RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 727-765 AND 1121-1145.
 RC TISSUE=Platelet;
 RX MEDLINE=95255215; PubMed=7737110;
 RA Reinhard M., Giehl K., Abel K., Haffner C., Jarchau T., Hoppe V.,
 RA Jockusch B.M., Walter U.;
 RT "The proline-rich focal adhesion and microfilament protein VASP is a
 RT ligand for profilins.";
 RL EMBO J. 14:1583-1589(1995).
 CC -!- FUNCTION: Binds to GTP-bound form of Rho and to profilin. Acts in
 CC a Rho-dependent manner to recruit profilin to the membrane, where
 CC it promotes actin polymerization. It is required for cytokinesis,
 CC stress fiber formation, and transcriptional activation of the
 CC serum response factor. DRF proteins couple Rho and Src tyrosine
 CC kinase during signaling and the regulation of actin dynamics (By
 CC similarity). In hearing it may play a role in the regulation of
 CC actin polymerization in hair cells.
 CC -!- TISSUE SPECIFICITY: Expressed in brain, heart, placenta, lung,
 CC kidney, pancreas, liver, skeletal muscle and cochlea.
 CC -!- DOMAIN: DRFs are regulated by intramolecular GBD-DAD binding where
 CC Rho-GTP activates the DRFs by disrupting the GBD-DAD interaction
 CC (By similarity).
 CC -!- DISEASE: Defects in DIAPH1 are a cause of autosomal dominant
 CC nonsyndromic sensorineural deafness 1 (DFNA1) [MIM:124900].
 CC -!- SIMILARITY: Contains 1 GTPase-binding (GBD) domain.
 CC -!- SIMILARITY: Contains 1 Formin homology 1 (FH1) domain.
 CC -!- SIMILARITY: Contains 1 Formin homology 2 (FH2) domain.
 CC -!- SIMILARITY: Contains 1 Formin homology 3 (FH3) domain.
 CC -!- SIMILARITY: Contains 1 DRF autoregulatory (DAD) domain.
 CC -!- SIMILARITY: Belongs to the formin homology family. Diaphanous
 CC subfamily.
 CC -!- CAUTION: Ref.2 sequence differs from that shown in that it seems
 CC to include intronic sequence.
 CC -!- DATABASE: NAME=Hereditary hearing loss homepage;
 CC NOTE=Gene page;
 CC WWW="http://www.uia.ac.be/dnalab/hhh/".
 CC -----
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 DR EMBL; AF051782; AAC05373.1; -.
 DR EMBL; AK023345; BAB14533.1; ALT_SEQ.
 DR Genew; HGNC:2876; DIAPH1.
 DR MIM; 602121; -.
 DR MIM; 124900; -.
 DR GO; GO:0007605; P:hearing; TAS.
 DR InterPro; IPR003104; FH2.
 DR Pfam; PF02181; FH2; 1.
 DR SMART; SM00498; FH2; 1.

Qy 222 -----SFRI-----YKGVIAIQKS 236
 | | | |:
 Db 958 LVGNMAGSRNAGAFGFNISFLCKLRDTKSTDQKMTLLHFLAELCENDYPDVLKF---P 1014

 Qy 237 DEGHPPFRAYLESEVAISEELVQK----- 259
 || |::| :| | :||
 Db 1015 DE---LAHVEKASRVSAENLQKNLDQMKKQISDVERDVQNFPAATDEKDKFVEKMTSEV 1070

 Qy 260 -----YSNSALGHVN--CTIKEL-----RRLFL----- 280
 |: : | | ||| | :||
 Db 1071 KDAQEQYNKLRRMMHSNMETLYKELGEYFLFDPKKLSVEEFFMDLHNFRNMFLQAVKENQK 1130

 Qy 281 -----VDDLVDSLKFAVIMWV 296
 :| |::|:
 Db 1131 RRKTEEMRRAKLAKEKAERLEKQKREQLIDMNAEGDETGVMDSLLEALQ----- 1183

 Qy 297 FTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG-----LANKNVK-DAMAKI 349
 || | :| | : | ||:: | ||| :
 Db 1184 ---SGAAFR-----RKRGPQANRKAGCAVTSLLASELTKDDAMAASV 1222

 Qy 350 QAKI-----PGLKRKAE 361
 ||: | : :|:
 Db 1223 PAKVSKNSETFPTILEEAK 1241

Search completed: September 29, 2004, 18:52:12
 Job time : 20.0208 secs